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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:45:41 ; Search time 182 Seconds
(without alignments)
2841.201 Million cell updates/sec

Title: US-09-516-728A-4
Perfect score: 7030
Sequence: 1 MKPARAPARLPSPGRLRW.....TIYENLAPVTTFKNGYIA 1337

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7030	100.0	1337	7	ADL16193
2	7030	100.0	1337	8	ADP74603
3	6950	98.9	1337	7	ADL16195
4	6824	97.1	1337	2	AAK85203
5	4508.5	64.1	1238	7	ADL16198
6	4499.5	64.0	1216	7	ADL16200
7	1811	25.8	341	8	ADP74604
8	1259.5	17.9	1998	7	AAO24268
9	1242	17.7	1997	3	AAAB19774
10	1242	17.7	1997	4	AAAM78821
11	1242	17.7	1997	8	ADOO4580
12	1241	17.7	1997	5	AAE20278
13	1241	17.7	1997	7	ABR57179
14	1241	17.7	1997	7	ADJ70329
15	1241	17.7	2002	4	AAAM79805
16	1230	17.5	1450	7	ABR57182
17	1177.5	16.7	1115	8	ADN12200
18	1140	16.2	1128	8	ABM82538
19	1130	16.1	1118	6	ABR43689
20	1127	16.0	1093	6	ABR43689
21	1124.5	16.0	1099	8	ABM82535
22	1112	15.8	1102	8	ABE28325
23	1107.5	15.8	1083	8	ABM82537
24	1105	15.7	1128	8	ABM82533
25	1101	15.7	1531	7	ADBO8753

26	1088	15.5	1112	8	ABM82534	Abm82534 Human dia
27	1079	15.3	1084	4	ABM82536	Abm82536 Human dia
28	1043.5	14.8	1647	4	ABM84428	Abm84428 Drosophila
29	993.5	14.1	579	3	ABAB19773	Abab19773 Mouse vas
30	991.5	14.1	1705	5	ABR52348	Abbr52348 Protein r
31	969	13.8	1767	4	ABR62726	Abbr62726 Drosophila
32	957.5	13.6	1711	5	ABR52349	Abbr52349 Protein r
33	954	13.6	1711	2	AAW70506	AAw70506 Osteoclast
34	944	13.4	1711	2	AAW70507	AAw70507 Mutant os
35	924.5	13.2	1447	7	ABR57181	Abbr57181 Drosophila
36	889.5	12.7	336	8	ADOO4582	Adoo4582 Human HPT
37	879	12.5	1912	8	ADRA40183	Adra40183 Human pro
38	878.5	12.5	312	8	ADOO4584	Adoo4584 Human HPT
39	878.5	12.5	319	6	ADOO4585	Adoo4585 Human HPT
40	864	12.3	2301	6	ABP60058	Abp60058 Human pho
41	855	12.2	1188	2	AAW42991	AAw42991 Amino aci
42	854	12.1	1188	5	ABR52338	Abbr52338 Protein r
43	854	12.1	1188	7	ADDB89075	Addb89075 TAT79. 1
44	854	12.1	1188	8	ADSL1078	Adsl1078 Human 207
45	849.5	12.1	1217	7	ADD46195	Add46195 Rat Procte

ALIGNMENTS

RESULT 1	ADL16193	standard; protein, 1337 AA.
XX	ADL16193;	
XX	ADL16193;	
XX	06-MAY-2004	(first entry)
XX		
DE	Human protein tyrosine phosphatase #13.	
XX	cytosolic; immunosuppressive; antiallergic;	
KW	protein tyrosine phosphatase; reversible oxidation;	
KW	inducible signalling pathway; cell proliferation; cancer;	
KW	guest vs. host disease; autoimmune disease; allergy; metabolic disorder;	
KW	cell-cycle abnormality; enzyme.	
OS	Homo sapiens.	
XX	MO2003068984-A2.	
XX	21-AUG-2003.	
XX	13-FEB-2003; 2003WO-EP001446.	
XX	13-FEB-2002; 2002US-0356810P.	
PR	12-FEB-2003; 2003US-00366547.	
XX	(COLD-) COLD SPRING HARBOR LAB.	
PA	(CEPT-) CEPTYR INC.	
XX	Tonks NK, Tzu-Ching M, Cool DE;	
XX	WPI; 2003-712572/67.	
DR	N-PSDB; ADL16192.	
PT	Identifying reversibly oxidized protein tyrosine phosphatase, useful in	
PT	screening for specific modulators, potential agents for treating e.g.	
PT	cancer or autoimmune disease.	
XX	Disclosure; SEQ ID NO 42; 23Bpp; English.	
PS	The invention relates to a method for identifying a protein tyrosine	
CC	phosphatase (PTP) that is reversibly oxidized in a cell by: (i)	
CC	subjecting a sample, including a cell that contains at least one PTP, to	
CC	conditions that cause reversible oxidation of PTP; (ii) isolating PTP	
CC	aneuridically, in presence of a sulhydryl-reactive agent (IR) that	
CC	irreversibly modifies the thiol group of an invariant Cys in the active	
CC	site of PTP; and (iii) determining, under reducing conditions, the level	

of dephosphorylation, caused by PTP, of a labelled substrate (11), where
 CC dephosphorylation indicates that an active PTP is present. No details
 CC of tests for these activities are given. The method is used to identify
 CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
 CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
 CC are involved. These agents are potentially useful, in human or veterinary
 CC medicine, for treating abnormal cell proliferation or growth (cancer);
 CC guest vs. host diseases; autoimmune diseases; allergy or other
 CC immunosuppressed states; metabolic disorders and cell-cycle
 CC abnormalities. This sequence represents one of the PTP enzyme of the
 CC invention.

XX Sequence 1337 AA;

Query Match 100.0%; Score 7030; DB 7; Length 1337;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPAREARLPSPSPGLRWALPLLLLLRLGQILCAGTSPSP1PPPSVATVATGNGITQ 60
 DB 1 MKPAREARLPSPSPGLRWALPLLLLLRLGQILCAGTSPSP1PPPSVATVATGNGITQ 60
 QY 61 ISSIASFHKONGTGPQVEITVISEDSSGANDSLRPEOGSNGTDGASQKTPSTGPS 120
 DB 61 ISSIASFHKONGTGPQVEITVISEDSSGANDSLRPEOGSNGTDGASQKTPSTGPS 120
 QY 121 PVPDIKAVSISPTNYLLTWKSNDAASEKYVVKHMEKITTIVHQPWCNITGLRAT 180
 DB 121 PVPDIKAVSISPTNYLLTWKSNDAASEKYVVKHMEKITTIVHQPWCNITGLRAT 180
 QY 181 SYVFSITPGIGNETWGDPRVIVKITEPIVSDLRVALTGVRKALSMWNGNGTASCRVLL 240
 DB 181 SYVFSITPGIGNETWGDPRVIVKITEPIVSDLRVALTGVRKALSMWNGNGTASCRVLL 240
 QY 241 BSIGSHEELTOUSRLQVNIISDLKRGVQVNIINPYLLQSNKTKDDPIGTGCGLDASTERSR 300
 DB 241 BSIGSHEELTOUSRLQVNIISDLKRGVQVNIINPYLLQSNKTKDDPIGTGCGLDASTERSR 300
 QY 301 AGSPAPVHDESLVGPVDPSSGQSRDTEVLLVGLPEGTRVAVATVYSGAANGTEGQPOAI 360
 DB 301 AGSPAPVHDESLVGPVDPSSGQSRDTEVLLVGLPEGTRVAVATVYSGAANGTEGQPOAI 360
 QY 361 EFRRTAIOVFDTAVANISATSLTLIMKVSNDNESSNNTYKIHVAGETDSNLIANSEPRAY 420
 DB 361 EFRRTAIOVFDTAVANISATSLTLIMKVSNDNESSNNTYKIHVAGETDSNLIANSEPRAY 420
 QY 421 IPGLASSTFVNITVCPVLGDIETGPGFLOVHTPPVPVSDFRVAVSTTEIGLAWSSHDAE 480
 DB 421 IPGLASSTFVNITVCPVLGDIETGPGFLOVHTPPVPVSDFRVAVSTTEIGLAWSSHDAE 480
 QY 481 SFQWHTIOEGAGNSRVEITTNOSIIIGGLPGTKYCFEIVKRGPNTEGASRTVCNRTVP 540
 DB 481 SFQWHTIOEGAGNSRVEITTNOSIIIGGLPGTKYCFEIVKRGPNTEGASRTVCNRTVP 540
 QY 541 SAVPDIHVYVVTTEMLDMKSPDGASRYVHLVYESKSGNSHTSTYDKAITLQGLIPGT 600
 DB 541 SAVPDIHVYVVTTEMLDMKSPDGASRYVHLVYESKSGNSHTSTYDKAITLQGLIPGT 600
 QY 601 LYNITISPEVDHVMGDPNSTAQYTRPSNVSNIDVSTNTAATLSMONDDASPTYSYCL 660
 DB 601 LYNITISPEVDHVMGDPNSTAQYTRPSNVSNIDVSTNTAATLSMONDDASPTYSYCL 660
 QY 661 IEKAGNSSNATQVVTIDIGITDAYTELI PGSSYVEIFPAQVGDIKSLERPKRSFCTDPA 720
 DB 661 IEKAGNSSNATQVVTIDIGITDAYTELI PGSSYVEIFPAQVGDIKSLERPKRSFCTDPA 720
 QY 721 SMA5FDCVAVKEPRLVWKTCPPGANA GFLEVS SGAMNNA TLBESSCNGTEYRETV 780
 DB 721 SMA5FDCVAVKEPRLVWKTCPPGANA GFLEVS SGAMNNA TLBESSCNGTEYRETV 780
 QY 781 TYLNFSTSYNISITTVSCGKMAAFTRNCTGTGIDPPPDSPNITSVSHNSVYVKRSGF 840
 DB 781 TYLNFSTSYNISITTVSCGKMAAFTRNCTGTGIDPPPDSPNITSVSHNSVYVKRSGF 840

QY 841 EASHSPRIYAVIILTTGAGHPSPADVLKTYTDFDKGASDTYTYLLIRTEKGRSOSLSB 900
 DB 841 EASHSPRIYAVIILTTGAGHPSPADVLKTYTDFDKGASDTYTYLLIRTEKGRSOSLSB 900
 QY 901 VLKREIDVGNSTLLGYNGKLEPLSGYRACVAFNTITFHPOKGLIDGAE5YVSRSY 960
 DB 901 VLKREIDVGNSTLLGYNGKLEPLSGYRACVAFNTITFHPOKGLIDGAE5YVSRSY 960
 QY 961 SDAVSLPDQPGVICGAVFGCIFGALVIVTVOGFIEMRKERKADANNVSVSQAIPKSKL 1020
 DB 961 SDAVSLPDQPGVICGAVFGCIFGALVIVTVOGFIEMRKERKADANNVSVSQAIPKSKL 1020
 QY 1021 IRVENFEAFYFKQOADSNCGFAEYEDLKVGISQPKYAELENNRKNRNVL PYDIS 1080
 DB 1021 IRVENFEAFYFKQOADSNCGFAEYEDLKVGISQPKYAELENNRKNRNVL PYDIS 1080
 QY 1081 RVKLSVOTHSITDDYINANNMFGYHSKKDPIATQGPLPNTLKDFRMVMEKNVVAIIMLT 1140
 DB 1081 RVKLSVOTHSITDDYINANNMFGYHSKKDPIATQGPLPNTLKDFRMVMEKNVVAIIMLT 1140
 QY 1141 CVEQARTKCEBYWPSKQADYGDITVAMTSEIVLPEWTRDFTVKNIQTESHPLRQFHF 1200
 DB 1141 CVEQARTKCEBYWPSKQADYGDITVAMTSEIVLPEWTRDFTVKNIQTESHPLRQFHF 1200
 QY 1201 TSWPDHGVPTDILLINFRILVNDYMKQSPPEPILVHGAGYGRGTPTAIDRLIYOIE 1260
 DB 1201 TSWPDHGVPTDILLINFRILVNDYMKQSPPEPILVHGAGYGRGTPTAIDRLIYOIE 1260
 QY 1261 NENTVDYGIYDLMRPLMVGTEPDQYVFLNCCVLDIVSOKSDKVDLYONTTAMTY 1320
 DB 1261 NENTVDYGIYDLMRPLMVGTEPDQYVFLNCCVLDIVSOKSDKVDLYONTTAMTY 1320
 QY 1321 ENLAPVTTFGKNGYIA 1337
 DB 1321 ENLAPVTTFGKNGYIA 1337

RESULT 2
 ADP74603
 ID ADP74603 standard; protein; 1337 AA.
 XX
 AC ADP74603;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Amino acid sequence of human DEP-1.
 XX
 KW human; density enhanced phosphatase-1; DEP-1; DEP-1 complex;
 KW p120 catenin; adaptor protein; Gab 1; hepatocyte growth factor receptor;
 KW HGF receptor; scatter factor receptor; SF receptor; Met; plakoglobin;
 KW beta-catenin; signal transduction; cell growth; cell proliferation;
 KW cell cycle regulation; contact inhibition; cellular differentiation;
 KW cellular morphogenesis; cellular motility; cytoskeleton.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048549-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038089.
 XX
 PR 26-NOV-2002; 2002US-0429746P.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Palaka-Hambliin HL, Tonks NK;
 XX
 DR WPI: 2004-450367/42.
 DR N-PDSB; ADP74602.
 XX
 PT New isolated complex comprises Density Enhanced Phosphatase-1 (DEP-1)

PT polypeptide, useful for manipulating biological signal transduction
 PT pathways, or determining additional molecular components of the pathways.
 XX
 PS Claim 2; Page 95-97; 130pp; English.

XX The present sequence represents a human density enhanced phosphatase-1
 CC (DEP-1) polypeptide. The specification describes DEP-1 complexes,
 CC comprising DEP-1 and DEP-1 substrates. DEP-1 substrate polypeptides that
 CC interact specifically with the substrate-trapping mutant form of DEP-1
 CC are isolated from human breast tumour cell lines. These polypeptides
 CC include the functional component of p120 catenin, the adaptor protein Gab
 CC 1, the hepatocyte growth factor (HGF)/scatter factor (SF) receptor Met, a
 CC plakoglobin polypeptide, and a beta-catenin polypeptide. The DEP-1
 CC complexes are useful for manipulating biological signal transduction
 CC pathways, including defining therapeutic targets, or determining
 CC additional molecular components of such pathways. Agents which modulate
 CC the complexes are useful for therapeutic interventions which influence
 CC biological processes, e.g. cell growth or proliferation including cell
 CC cycle regulation and contact inhibition of cell growth, cellular
 CC differentiation including altered cellular morphogenesis or motility or
 CC other cellular activities characterized by alterations in cytoskeletal
 CC organization and/or cellular gene expression, or cell survival including
 CC cellular responses to apoptotic stimuli.

XX Sequence 1337 AA:

Query Match 100.0%; Score 7030; DB 8; Length 1337;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPARARARLPSPGRLMALPLLLLLRLGQILCAGTSPSPIDPPSVATVATGNGITQ 60
 DB 1 MKPARARARLPSPGRLMALPLLLLLRLGQILCAGTSPSPIDPPSVATVATGNGITQ 60
 QY 61 ISSAESFHKONGTGPQVETNTSEDGSSGANDSLRTPGQSGNGTDGASQKTPSSTPS 120
 DB 61 ISSAESFHKONGTGPQVETNTSEDGSSGANDSLRTPGQSGNGTDGASQKTPSSTPS 120
 QY 121 PVPIKAVSISPTNVILTWKNDTRASRYKYVGHKMKENKTIIVVHQPCNITIGLRPAT 180
 DB 121 PVPIKAVSISPTNVILTWKNDTRASRYKYVGHKMKENKTIIVVHQPCNITIGLRPAT 180
 QY 121 PVPIKAVSISPTNVILTWKNDTRASRYKYVGHKMKENKTIIVVHQPCNITIGLRPAT 180
 DB 121 PVPIKAVSISPTNVILTWKNDTRASRYKYVGHKMKENKTIIVVHQPCNITIGLRPAT 180
 QY 181 SYVSIITPGIGNETWGPDRVIAKITEPIVSDLRVALTGVRKAALSMNGNGTASCRVLL 240
 DB 181 SYVSIITPGIGNETWGPDRVIAKITEPIVSDLRVALTGVRKAALSMNGNGTASCRVLL 240
 QY 241 ESIGSHEELTQDSRLQVNIIDLKPGVOYNINPYLLQSNKTKGDPGLGEGGLDASNTESR 300
 DB 241 ESIGSHEELTQDSRLQVNIIDLKPGVOYNINPYLLQSNKTKGDPGLGEGGLDASNTESR 300
 QY 301 AGSPTPAPVHDESLVGPVDPSSGQOSRDTEVLLGLFEGTRNATVYSGAANGTEGQPOAI 360
 DB 301 AGSPTPAPVHDESLVGPVDPSSGQOSRDTEVLLGLFEGTRNATVYSGAANGTEGQPOAI 360
 QY 361 BFRFNAIOVFVTVNATISATSLTLIMKYSDNESSNATYKLVHAGETSSMLNVEPRAY 420
 DB 361 BFRFNAIOVFVTVNATISATSLTLIMKYSDNESSNATYKLVHAGETSSMLNVEPRAY 420
 QY 421 IPGRSSSTFYNTVCPVLGDIETPGFLQVATPPVPSDFRVTVVSTTEIGLAWSHDAE 480
 DB 421 IPGRSSSTFYNTVCPVLGDIETPGFLQVATPPVPSDFRVTVVSTTEIGLAWSHDAE 480
 QY 481 SFQWHTIOEGAGNSRVEITTNQSIIGLFPETKTCFEIVKRGNGTGCARTVCNRVTP 540
 DB 481 SFQWHTIOEGAGNSRVEITTNQSIIGLFPETKTCFEIVKRGNGTGCARTVCNRVTP 540
 QY 541 SAVFDIHVVYVVTTEMLDMKSPDGASEYVYHLVIESGHGSHNTSTYKATITLOGLIPGT 600
 DB 541 SAVFDIHVVYVVTTEMLDMKSPDGASEYVYHLVIESGHGSHNTSTYKATITLOGLIPGT 600
 QY 601 LYNITISPEVDHVGDPNSTAQYTRPSNVSNIDVSTNTAAATLSQWQNDASPTYSYCLL 660
 DB 601 LYNITISPEVDHVGDPNSTAQYTRPSNVSNIDVSTNTAAATLSQWQNDASPTYSYCLL 660

QY 661 IEKAGNSNATQVYTDIGITDATVTELLPGSSYVEIFAQVGDGIKSLERPKSFCTDPA 720
 DB 661 IEKAGNSNATQVYTDIGITDATVTELLPGSSYVEIFAQVGDGIKSLERPKSFCTDPA 720
 QY 721 SMASFDCEVVPKEBALVAKTCCPGANAGFELEVSAGANNATLIESCSSNGTEYRTVEV 780
 DB 721 SMASFDCEVVPKEBALVAKTCCPGANAGFELEVSAGANNATLIESCSSNGTEYRTVEV 780
 QY 781 TYLNFSTSYNISTITTVSCGKMAATRTCTTGITDPPPPGSPNITSVSHSVYVKSGF 840
 DB 781 TYLNFSTSYNISTITTVSCGKMAATRTCTTGITDPPPPGSPNITSVSHSVYVKSGF 840
 QY 841 EASHGPVKAVALITTEAGHPSADVLYKTYTDDPKKASDPTVYVYLLIRTEBKGSQSLSE 900
 DB 841 EASHGPVKAVALITTEAGHPSADVLYKTYTDDPKKASDPTVYVYLLIRTEBKGSQSLSE 900
 QY 901 VLKYEIDVGNESSTLYGYNGLBPLGSRACVAGFTNITPHQNGLIIDGASVVSFRY 960
 DB 901 VLKYEIDVGNESSTLYGYNGLBPLGSRACVAGFTNITPHQNGLIIDGASVVSFRY 960
 QY 961 SDAVSLPQDDPGVIGAVFGCIFGALVIVYVGFIEMKKRRDADKNEVSFSQIKPKSKL 1020
 DB 961 SDAVSLPQDDPGVIGAVFGCIFGALVIVYVGFIEMKKRRDADKNEVSFSQIKPKSKL 1020
 QY 1021 IRVENFEAYFKQOADSNCGFAEYEDLKVGISQPKYAAELANRGKRRYNNVLPYDIS 1080
 DB 1021 IRVENFEAYFKQOADSNCGFAEYEDLKVGISQPKYAAELANRGKRRYNNVLPYDIS 1080
 QY 1081 RVKLSVQTHSTDYINANNYMGYHKKDFIATQGPLPNTLKDFFRMWKKXNVAIIMLT 1140
 DB 1081 RVKLSVQTHSTDYINANNYMGYHKKDFIATQGPLPNTLKDFFRMWKKXNVAIIMLT 1140
 QY 1141 CVEGRTKCEBYWSSKQADYGDITVAMTSEIVLPETINDFTYKNIQTSSSHLRQPHF 1200
 DB 1141 CVEGRTKCEBYWSSKQADYGDITVAMTSEIVLPETINDFTYKNIQTSSSHLRQPHF 1200
 QY 1201 TSWPDHGVPTDILLINFRYLVRDYMKOSPESPILVHCSAGVGTGFIAIDRLIYOIE 1260
 DB 1201 TSWPDHGVPTDILLINFRYLVRDYMKOSPESPILVHCSAGVGTGFIAIDRLIYOIE 1260
 QY 1261 NENTVDYVGIYVLDLMMRPLMVQTEQDQVFLNQCVLDIRSQKSKVDLIYQNTTAMT 1320
 DB 1261 NENTVDYVGIYVLDLMMRPLMVQTEQDQVFLNQCVLDIRSQKSKVDLIYQNTTAMT 1320
 QY 1321 ENLAPVTTFGKTNGYIA 1337
 DB 1321 ENLAPVTTFGKTNGYIA 1337

RESULT 3
 ADL16195
 ID ADL16195 standard; protein; 1337 AA.
 AC ADL16195;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human protein tyrosine phosphatase #14.
 XX
 KW cytosolic; immunosuppressive; anti-allergic;
 KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KW inducible signalling pathway; cell proliferation; cancer; cell
 KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KW cell-cycle abnormality; enzyme.
 XX
 OS Homo sapiens.
 XX
 EN WO2003068984-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-EP001446.

KM Density enhanced Type III receptor-like protein tyrosine phosphatase;
 KM hudep-1.
 XX
 OS Homo sapiens.
 XX MO9530008-A1.
 XX PD 09-NOV-1995.
 XX
 XX 03-MAY-1995; 95MO-US005512.
 XX
 XX 03-MAY-1994; 94US-00237940.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 PI Tonks NK, Oestman A;
 XX
 XX WPI; 1995-393079/50.
 DR N-PSDB; AAT06027.
 XX
 PT New density enhanced protein tyrosine phosphatase - used to develop
 PT prods. to modify transcription, translation and activity of tyrosine
 PT phosphatase(s).
 PS
 PS Claim 4; Page 34-38; 51pp; English.
 XX
 CC A cDNA clone was obtd. (see AAT06027) from a HeLa cell cDNA library that
 CC encoded a novel density-enhanced Type III receptor-like FIP, designated
 CC hudep-1 (AAR5203). hudep-1 is useful for the study of PTs and for the
 CC development of therapeutic or prophylactic cpds. e.g. for prevention of
 CC abnormal or malignant cell growth
 CC
 XX Sequence 1337 AA.

Query Match 97.1%; Score 6824; DB 2; Length 1337;
 Best Local Similarity 97.4%; Pred. No. 0;
 Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;

QY 1 MKPAAERARLPBRPGLRMLPLLLLRLLGQILCAGTSPSPIDPSVATVATGNGITQ 60
 DB 1 MKPAREARLPBRPGLRMLPLLLLRLLGQILCAGTSPSPIDPSVATVATGNGITQ 60
 QY 61 ISSAESFHKONGTGPVEINTSEDESGANDSLRTEQSGNGTDGASQKTPSSTPS 120
 DB 61 ISSAESFHKONGTGPVEINTSEDESGANDSLRTEQSGNGTDGASQKTPSSTPS 120
 QY 121 PVFPIKAVSISPTNVLTKMSNDTAASEKYVVKHKNKXTITVHQPMCNITGLRPA 180
 DB 121 PVFPIKAVSISPTNVLTKMSNDTAASEKYVVKHKNKXTITVHQPMCNITGLRPA 180
 QY 181 SYVESITPGIGNETWGDPRVTKVTEPIVSGDLRYALTGVKALSMNGNGTASCRVLL 240
 DB 181 SYVESITPGIGNETWGDPRVTKVTEPIVSGDLRYALTGVKALSMNGNGTASCRVLL 240
 QY 241 ESTGSHEELTODSLQVNIISDLKPGVOYNINPYLLQSKTKGDPGLTEGGLDASTEKSR 300
 DB 241 ESTGSHEELTODSLQVNIISDLKPGVOYNINPYLLQSKTKGDPGLTEGGLDASTEKSR 300
 QY 301 AGSFAPVHDESLVGVDPSSGQSRDTEVLLVGLPESTRYNATVYSGAANGTEGQPAI 360
 DB 301 AGSFAPVHDESLVGVDPSSGQSRDTEVLLVGLPESTRYNATVYSGAANGTEGQPAI 360
 QY 361 EFRFNAIOVFVTAVNISATSLTLIMKYSDNESSNNTYKTHVAGETSSNLNVEPRAY 420
 DB 361 EFRFNAIOVFVTAVNISATSLTLIMKYSDNESSNNTYKTHVAGETSSNLNVEPRAY 420
 QY 421 IPRGRSSTFYNIITCPVLGDIETGPGFLQVHTPPVPSDFRYTVVSTTEIGLANSRAB 480
 DB 421 IPRGRSSTFYNIITCPVLGDIETGPGFLQVHTPPVPSDFRYTVVSTTEIGLANSRAB 480
 QY 481 SFQNHITDEGAGNSRVEITTNQSIIGGLPFGTKYCFEIVKPGNGTEGASRTVCNRTVP 540
 DB 481 SFQNHITDEGAGNSRVEITTNQSIIGGLPFGTKYCFEIVKPGNGTEGASRTVCNRTVP 540

QY 541 SAVFDIHVVYTTTMMMLDMKSPDGASEYVYHLVIESKHGSHNTSTYDKAITLQGLIPGT 600
 DB 541 SAVFDIHVVYTTTMMMLDMKSPDGASEYVYHLVIESKHGSHNTSTYDKAITLQGLIPGT 600
 QY 601 LYNITISPEVDHVGDNSTAQYTRPSNVSNIDVSTNTTAATLSWONPDASPTYSYCLL 660
 DB 601 LYNITISPEVDHVGDNSTAQYTRPSNVSNIDVSTNTTAATLSWONPDASPTYSYCLL 660
 QY 661 IEKAGNSNATQVYTDGITDATYTELIPGSSYVVELPAQVGDGIKSLPERKSPCTDPA 720
 DB 661 IEKAGNSNATQVYTDGITDATYTELIPGSSYVVELPAQVGDGIKSLPERKSPCTDPA 720
 QY 721 SMASFDECVAPKEPALVLMKTCPPGANAGFELVSSGAMNNATLIESCSENGETEYRTEV 780
 DB 721 SMASFDECVAPKEPALVLMKTCPPGANAGFELVSSGAMNNATLIESCSENGETEYRTEV 780
 QY 781 TYLNFSTSYNISITTVSCGKMAAPTRNTCTGTITDPPPDGSPNITSVSHNSVVKSGF 840
 DB 781 TYLNFSTSYNISITTVSCGKMAAPTRNTCTGTITDPPPDGSPNITSVSHNSVVKSGF 840
 QY 841 EASHGPIKAYAVILITGBAGHPSADVLYKTYDDPKKASDPTVYTYLLRTEKGRSQSLSE 900
 DB 841 EASHGPIKAYAVILITGBAGHPSADVLYKTYDDPKKASDPTVYTYLLRTEKGRSQSLSE 900
 QY 901 VLKYEIDVGNSESTLGYNGKLBPGLSFRACVAGFTNITFHPONKGLIDGASVVSFSRY 960
 DB 901 VLKYEIDVGNSESTLGYNGKLBPGLSFRACVAGFTNITFHPONKGLIDGASVVSFSRY 960
 QY 961 SDAVSLPQDPGVICGAVFGCIFGALVITVGGFIFMRKKRKDAKONEVVSFOIKPKSKL 1020
 DB 961 SDAVSLPQDPGVICGAVFGCIFGALVITVGGFIFMRKKRKDAKONEVVSFOIKPKSKL 1020
 QY 1021 IRVENFEAYFKKQADNSNCGFAEYEDLKLVGISQPKYAAELANRGNRNNTLPYDIS 1080
 DB 1021 IRVENFEAYFKKQADNSNCGFAEYEDLKLVGISQPKYAAELANRGNRNNTLPYDIS 1080
 QY 1081 RVKLSVQTHSTDDYINANNYMGYHSKKDFIATQGPLPNTLKDFMRMWEKVVVAILMLTK 1140
 DB 1081 RVKLSVQTHSTDDYINANNYMGYHSKKDFIATQGPLPNTLKDFMRMWEKVVVAILMLTK 1140
 QY 1141 CVEQGRTKCEBYEWSKOADYDGIITVAMTSEIVLPEWTRIDFTYKNIQTSSHPLRQHF 1200
 DB 1141 CVEQGRTKCEBYEWSKOADYDGIITVAMTSEIVLPEWTRIDFTYKNIQTSSHPLRQHF 1200
 QY 1201 TSWPDHGVPTDILLINFRYLVRDYMKQSPRESILVHCSAGVGRGTGFIAIDRLIYQIE 1260
 DB 1201 TSWPDHGVPTDILLINFRYLVRDYMKQSPRESILVHCSAGVGRGTGFIAIDRLIYQIE 1260
 QY 1261 NENTVDVYGIYDILRMHRPLMVOTEDQYVFINQCVLDIIVSOKSKVDLLIYQNTTAMTIY 1320
 DB 1261 NENTVDVYGIYDILRMHRPLMVOTEDQYVFINQCVLDIIVSOKSKVDLLIYQNTTAMTIY 1320
 QY 1321 ENLAPVTTFGKTNGYIA 1337
 DB 1321 ENLAPVTTFGKTNGYIA 1337

RESULT 5
 ADL16198
 ID ADL16198 standard; protein; 1238 AA.
 XX
 AC ADL16198;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Mouse protein tyrosine phosphatase #4.
 XX
 XX cytosolic; immunosuppressive; antiallergic;
 KM protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
 KM inducible signalling pathway; cell proliferation; cancer;
 KM guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
 KM cell-cycle abnormality; enzyme.

ID ADL16200 standard; protein; 1216 AA.
XX
AC ADL16200;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat protein tyrosine phosphatase #4.
XX
KW cytosolic; immunosuppressive; antiallergic;
KW protein tyrosine phosphatase; reversible oxidation; dephosphorylation;
KW inducible signalling pathway; cell proliferation; cancer;
KW guest vs. host disease; autoimmune disease; allergy; metabolic disorder;
KW cell-cycle abnormality; enzyme.
XX
OS Rattus norvegicus.
XX
PN WO2003068984-A2.
XX
PD 21-AUG-2003.
XX
PE 13-FEB-2003; 2003WO-EP001446.
XX
PR 13-FEB-2002; 2002US-0356810P.
XX
PR 12-FEB-2003; 2003US-00366547.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI (CEPT-) CEPTYR INC.
XX
PI Tonks NK, Tzu-Ching M, Cool DE;
XX
DR WPI; 2003-712572/67.
XX
DR N-PSDB; ADL16199.
XX
PT Identifying reversibly oxidized protein tyrosine phosphatase, useful in
PT screening for specific modulators, potential agents for treating e.g.
PT cancer or autoimmune disease.
XX
PT
XX
PS Disclosure; SEQ ID NO 49; 238pp; English.
XX
CC The invention relates to a method for identifying a protein tyrosine
CC phosphatase (PTP) that is reversibly oxidized in a cell by: (1)
CC subjecting a sample, including a cell that contains at least one PTP, to
CC conditions that cause reversible oxidation of PTP; (ii) isolating PTP
CC anaerobically, in presence of a sulfhydryl-reactive agent (ii) that
CC irreversibly modifies the thiol group of an invariant Cys in the active
CC site of PTP; and (iii) determining, under reducing conditions, the level
CC of dephosphorylation, caused by PTP, of a labelled substrate (iii), where
CC dephosphorylation indicates that an active PTP is present. No details
CC of tests for these activities are given. The method is used to identify
CC reversibly oxidized PTP, also to identify agents that: (a) reversibly
CC modify such PTP; or (b) alter inducible signalling pathways in which PTP
CC are involved. These agents are potentially useful, in human or veterinary
CC medicine, for treating abnormal cell proliferation or growth (cancer);
CC guest vs. host disease; autoimmune disease; allergy or other
CC immunosuppressed states; metabolic disorders and cell-cycle
CC abnormalities. This sequence represents one of the PTP enzyme of the
CC invention.
XX
XX
SQ Sequence 1216 AA;
Query Match 64.0%; Score 4499.5; DB 7; Length 1216;
Best Local Similarity 67.1%; Pred. No. 5,2e-292;
Matches 900; Conservative 106; Mismatches 205; Indels 111; Gaps 10;

DB
42 PVFDVEAVT-SPTSVILTWKNDTSATSEYK-----NEGNTLRVYTKQNTSFNITGLSPAT 96
181 SYVSTIPGIGNETWGPBVKVITTEPIPVSDLAVALTGKALKSWNGNGTASCRLL 240
97 SYKPSITLGTVENETSGKRTYKNITTEPWPVSDLOVAIYIGVQALLMANAGTAKYRQI 156
241 ESIGSHEELTQDSRLQVNI SDLPKPGVOYNINPYLLQSNKTKGDDPLGTEGGDASNTSR 300
157 -----VELTNS--SGGISDLKKGTHKSL--AVQGSNETQHDLMYTE----- 194
301 AGSEPTAPVHDSILVGPVDPSSGQOSRDTEVLVLGLPCTR NATVYSGAANGTEGQPAI 360
195 -----GVSDPPSARDPSLTEVLITELKPDQTKYKVIYSGAADTEGQPGNK 240
361 EFRTNALQVPTVAVNISATSLTILKYSVDNESSNTYKIHVAGETDSSULANSEPAV 420
241 VFKNTPLOVSDIRAVNISDSNMTLTWKSNNSHASFYKLYVAGSGDSINETVNETQAV 300
421 IGLRSSTFYNIITVCPVLGDI EGTGPFLOVHTPPVPVSDPFRVTVSTTEIGLAMSHPDAE 480
301 IRLSSSTLNIITVLPFLGQTAGLPGFLQVTTSPRPVSDPRTVNSLREIGLARSNDSE 360
481 SPQNHITQEGAGNSRVELTTNQSIIGGLPFGTKYCEIIVKPGNGTEGASRTVCNRTVP 540
361 SFEIPIQEGSEKKMNASGTDLSYIVNLKGTSYQFPIPRCPNGTEGSPQTVVGRDTC 420
541 SAVFDIHVYVYTTTMMLDKMSPDGASBYVHLVYESHGNSHSTYDKATITLOGILPGT 600
421 SAVTDIRVAVSYTEILOEMQNTDSAGYTHLVLESNGSIKTNSSQKMTIVGGLPGT 480
601 LYNITISPEVDHVGMDPNSTAOQYTRPSNVSNIDVSTNTTAATLSMOPNDPASPTYSYCL 660
481 LYNVTIIPPEVDQMGKNSSTIQYTRPSNVSTIEVNTITVATIQKILDAASAYSISVL 540
661 IEKAGNSNATOVVTDIGITDATVTEILPGSSYVTEIF-----AQVGDGIXLEPRKRSF 715
541 ILKAGDSNVTISRARD--IPSVTIIGLIPGVSEVKLFTKIRNTEVGNV----PGQLGF 594
716 CTDPAASMAFPCCEVPVPPKALVLTWTCPPRANAGFELEVSAGANNATHLESCESENTE 775
595 CMEPAOVDSLCEVVPKPEPALVLTWACPPGNNSGFELGVSRDADNMTHLENCTLDNTE 654
776 YRTEVTYLNFTSTYNI STITVSGKMAAPRNTCTGTGIDPPDPGSPNITSVSHNSKV 835
655 CRTEVTYLNFTSTYNI STIATLSCRMALPTVSTCTGTGIDPPDPGSPNITSVSHNSKV 714
836 KFSGFESHGPIKAYAVILTTGEAGHPSADVLKTYTDPFKKASDVTYVTLIRTEKGRS 895
715 KFSGFESHGPIKAYAVILTTGEAGHPSADVLKTYTDPFKKASDVTYVTLIRTEKGRS 774
896 QSLSEVLKTEIDVGNESSTLTGYNGKLEPLGSTRACVAGFNITFHFNOKLIDGAEYV 955
775 QGLSEALNTEIDVGNOSTTGLGYNGRLEPLGSTRACVAGFNITYNQNDLINDGDESY 834
956 SESRYSAVSLPDOPGVICGAVPGCIFGALVTIVVGGIFPRKRRKDAKNNVESFSQIKP 1015
835 SFSPTSEAVSLPDOPGVICGAVPGCIFGALVTIVVGGIFPRKRRKDAKNNVESFSQIKP 894
1016 KKSRLIRVNEFEAYFKKQOADSNGCFABEYEDLKLVGISQPKYAAELAENGRKRYNNVL 1075
895 KKSRLIRVNEFEAYFKKQOADSNGCFABEYEDLKLIGSLPKYAAELAENGRKRYNNVL 954
1076 PYDISRYKLSYQHTSTDDYINANTMPGYHKKDPIATQGPILPNTLKDFMRVWKEKYAY 1135
955 PYDISRYKLSYQHTSTDDYINANTMPGYHKKDPIATQGPILPNTLKDFMRVWKEKYAY 1014
1136 IMLTKVCGKRTCKEEMWPSKOADYGDITYAAMSEIYLPMTTRDFTVKVNIQTSSEHPL 1195
1015 VMLTKVCGKRTCKEEMWPSKOADYGDITYAAMSEIYLPMTTRDFTVKVNMSSSEHPL 1074
1196 ROFHTSMPDHGVDPTDLDLINFRTYLVADYMKQSPSPSPILVHCSAGVGTGTEIAIDRL 1255

Db 1075 RQFHTSWPDHGVPTDITLLINFRYLVRDYMKQIPESPILVHCASVGRGTFTAIIDL 1134
 QY 1256 IYGIENENTVDYVGIYDLMRHPLMVQTEQYVFLNOCYLDIVSOKSKVDLIYQNTT 1315
 Db 1135 IYGIENENTVDYVGIYDLMRHPLMVQTEQYVFLNOCYLDIIRAKOSKVDLIYQNTT 1194
 QY 1316 AMTIYENLAPVTTEGKTNGYIA 1337
 Db 1195 AMTIYENLERSVWFGKANGYIA 1216

RESULT 7
 ADP74604
 ID ADP74604 standard; peptide; 341 AA.
 XX
 AC ADP74604;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Amino acid sequence of a human DEP-1 fragment.
 XX
 KW human; density enhanced phosphatase-1; DEP-1; DEP-1 complex;
 KW p120 catenin; adaptor protein; Gab 1; hepatocyte growth factor receptor;
 KW HGF receptor; scatter factor receptor; SF receptor; Met; plakoglobin;
 KW beta-catenin; signal transduction; cell growth; cell proliferation;
 KW cell cycle regulation; contact inhibition; cellular differentiation;
 KW cellular morphogenesis; cellular motility; cytoskeleton.
 XX
 OS Homo sapiens.
 XX
 PN WO2004048549-A2.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-NOV-2003; 2003WO-US038089.
 XX
 PR 26-NOV-2002; 2002US-0429746P.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Palaka-Hamblin HL, Tonke NK;
 XX
 DR WPI: 2004-450367/42.
 XX
 PT New isolated complex comprises Density Enhanced Phosphatase-1 (DEP-1)
 PT polypeptide, useful for manipulating biological signal transduction
 PT pathways, or determining additional molecular components of the pathways.
 PS
 Claim 2; Page 98; 130pp; English.

CC The present sequence represents a human density enhanced phosphatase-1
 CC (DEP-1) fragment, comprising residues 997-1337 of ADP74603. The
 CC specification describes DEP-1 complexes, comprising DEP-1 and DEP-1
 CC substrates. DEP-1 substrate polypeptides that interact specifically with
 CC the substrate-trapping mutant form of DEP-1 are isolated from human
 CC breast tumour cell lines. These polypeptides include the functional
 CC component of p120 catenin, the adaptor protein Gab 1, the hepatocyte
 CC growth factor (HGF)/scatter factor (SF) receptor Met, a plakoglobin
 CC polypeptide, and a beta-catenin polypeptide. The DEP-1 complexes are
 CC useful for manipulating biological signal transduction pathways,
 CC including defining therapeutic targets, or determining additional
 CC molecular components of such pathways. Agents which modulate the
 CC complexes are useful for therapeutic interventions which influence
 CC biological processes, e.g. cell growth or proliferation including cell
 CC cycle regulation and contact inhibition of cell growth, cellular
 CC differentiation including altered cellular morphogenesis or motility or
 CC other cellular activities characterized by alterations in cytoskeletal
 CC organization and/or cellular gene expression, or cell survival including
 CC cellular responses to apoptotic stimuli.
 CC
 XX Sequence 341 AA;
 SQ

Query Match 25.8%; Score 1811; DB 8; Length 341;

Best Local Similarity 100.0%; Pred. No. 1e-112;
 Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 997 RKKRDAKNNEVSFSQIKPKSKLIRVENFEAYFKKOAOBNGCFABEYEDLKLVGISOP 1056
 Db 1 RKKRDAKNNEVSFSQIKPKSKLIRVENFEAYFKKOAOBNGCFABEYEDLKLVGISOP 60
 QY 1057 KYAAELANRGNKNNYNNVLPYDISRVKLSVQTHSTDDYINANNYPGYSKKDPFATQGPL 1116
 Db 61 KYAAELANRGNKNNYNNVLPYDISRVKLSVQTHSTDDYINANNYPGYSKKDPFATQGPL 120
 QY 1117 PNTLKDFRWVMEQNVYAIITLTKVCGPRKCEYSPSKOAOYGGITAMSEIYLPE 1176
 Db 121 PNTLKDFRWVMEQNVYAIITLTKVCGPRKCEYSPSKOAOYGGITAMSEIYLPE 180
 QY 1177 WTIRDFTVKNIQTSESHPLRQFHTSWPDHGVPTDITLLINFRYLVRDYMKQIPESPIL 1236
 Db 181 WTIRDFTVKNIQTSESHPLRQFHTSWPDHGVPTDITLLINFRYLVRDYMKQIPESPIL 240
 QY 1237 VHCASVGRGTFTAIIDLRIYGIENENTVDYVGIYDLMRHPLMVQTEQYVFLNOCYL 1296
 Db 241 VHCASVGRGTFTAIIDLRIYGIENENTVDYVGIYDLMRHPLMVQTEQYVFLNOCYL 300
 QY 1297 DIVRSQKSKVDLIYQNTAMTIYENLAPVTTEGKTNGYIA 1337
 Db 301 DIVRSQKSKVDLIYQNTAMTIYENLAPVTTEGKTNGYIA 341

RESULT 8
 AAO24268
 ID AAO24268 standard; protein; 1998 AA.
 XX
 AC AAO24268;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Murine vascular endothelial-protein tyrosine phosphatase.
 XX
 KW Vascular endothelial protein-tyrosine phosphatase; VE-PTP; mouse; human;
 KW gene therapy; cyostatic; VE-cadherin; vascular endothelial-cadherin.
 XX
 OS Mus sp.
 XX
 PN WO2003084565-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 08-APR-2003; 2003WO-EP003645.
 XX
 PR 08-APR-2002; 2002EP-00007837.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Nawroth R, Deutsch U, Vestweber D, Shima DT, Golding M;
 XX
 DR WPI: 2003-804251/75.
 XX
 PT Use of the polypeptide comprising vascular endothelial-protein tyrosine
 PT phosphatase (VE-PTP) or the nucleic acid encoding the polypeptide for the
 PT manufacture of an agent for monitoring or modulating VE-cadherin mediated
 PT disorders.
 PS
 Example; Fig 2; Opp; English.

CC The present invention relates to a polypeptide comprising vascular
 CC endothelial-protein tyrosine phosphatase (VE-PTP) or its active fragment
 CC or effector, or the nucleic acid encoding the polypeptide or its
 CC effector, for use in the manufacture of an agent for monitoring or
 CC modulating VE-cadherin mediated processes or disorders. The polypeptide
 CC comprising vascular endothelial-protein tyrosine phosphatase (VE-PTP) or
 CC its active fragment or effector, or the nucleic acid encoding the
 CC polypeptide or its effector, is useful for the manufacture of an agent
 CC for monitoring or modulating VE-cadherin mediated processes or disorders,

XX WPI; 2001-476283/51.
DR N-PSDB; AAK51954.
XX
PT Nucleic acid encoding polypeptides with cytokine-like activities, useful
in diagnosis and gene therapy.
PS Claim 20; Page 3761-3764; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAK578323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1997 AA;
Query Match 17.7%; Score 1242; DB 4; Length 1997;
Best Local Similarity 29.6%; Pred. No. 2.2e-73;
Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
QY 123 FDIKAVSISPTNVLITKSNDDTAEEYKVVKHEKNEKITVHQPWCNITGLRPAISY 182
DB FDHVEVITKKNKNFIOTKSIP-----KSENE-----CVFVQVPGRLY 796
QY 183 VFSTITPIG-----NETGDRVIVKIVTBPVSDLRVALTGVRKAALSMNGNGTASGRV 238
DB SVVTYTSKGYEANEQ-GNGRTI-----PEPVKDLITLRNSTDIEDHYWTSANG----- 844
QY 239 LLESIGSHE--ELQDSRL-----QVNISDLKPGVQY-----NINPYLLSKNT 280
DB 845 ---DVQDEIQLFNDKMKVPPFHLVNTATERYRTSLTPGKQKILVLTISGVDQGSFPI 901
QY 281 KG-----DPLG-----TEGLDASN-----TERSRAGSPFAVHDESL 313
DB 902 EGFVPSAVKNIHISFGATDSLTVNMTPGGVDVSYVSAFRISQKVDSTIPKH----- 957
QY 314 VGPVDPSSGQGSRTLEVVLGEPGTRYNATVYQAANGTEGQQAIEFRNALQVEDYT 373
DB 958 -----VFHHTFRLLEAGBOYQIWIAS--VSGSLKQINIVVGRVTPASVQGV 1002
QY 374 AVN-ISATSLILIKVSDNESSNYTKIHVAGETDSNLVSEPR-----VTPGL 424
DB 1003 ADNAVSSYSLIVSKQKAGVAE---RYDILITLNGILLRNTSEBATTQKHFEDLTPGK 1059
QY 425 RSTFTVNTVCPVLGIEGTGFLQVHTPPVPSDFRTVVTTEIGLAWSHDAESFOM 484
DB 1060 K-----YKIQILTYSGGJFSKAGQTEERTVPAALVLDLRTENSTHLSFRWASGELSMY 1115
QY 485 HI---TOEGAGNSVEI--TTNQSIIGGLPFGTYCEIIVKGPNGTEGASRTVCNRTVP 540
DB 1116 NIFLYNPDGNLOERAQVDFIVQSFQNLQGRMYKWIIVH---SGELSNESPIFGRIVP 1173
QY 541 SAVVDIHVVVYVTTTE--WMLDKSPDASRYVYHVLVTSKHSNHTSYDKAIT---LQGL 596
DB 1174 ASVSHLGSNKNRNTDLSLTFMNSPASGDPDF--YELLINPNSTKKEKMKDKDLTEWRQGL 1232
QY 597 IPGTLVNTITSPEDVHWGDPNSTAOYTR-----PSNVSNIDVSTNTTATL---SNQN 647
DB 1233 VPGKRYLWV---VTHSGDLSNKTATASRTAPSPSLMSFADIANSTALATWKPBPWTD 1289
QY 648 FDDASPTY---SYCLLEKAGNSNATOVVTDIGITDATTTELLPGSSYVEIRAQVGDG 704
DB 1290 YNDFELQWLPRLDALTVNPNYNNRKESEGRIVYG-----LRPGRSYQFNVVTVSGDS 1339

QY 705 IKSL-EPGRKSFCTDPASMASFDCEVVPKEBPALVLTWTCPPGANAGELEVSSGAMNAT 763
DB 1340 WKTVSKPIFGSVTRKTPKIQNLHCR--PQNSTALICSMWIPDSDPDGYSIE-----CR 1390
QY 764 HLESCSENGTEVTEVYIYNF-----STSYNISITVSCGKMAAPRINTCTGTTDPP 818
DB 1391 KMDTQEVFESRKLEKEKESLNLIMLVPHKRYLVSIKVQSGAMTSEVEDSTTMDIDRPP 1450
QY 819 PDGSPNI-----TSVSHNSVK--VKFSGFASHGPIKAVAVILTTG-----EAGHP 862
DB 1451 P--PPIHNVKEDVLKSSINFTVNCSPWSDTNGAVKFTVVVVRADGSDLEKPEQHP 1508
QY 863 SADVLKTYDDFKKASDIYVYVILIRTEKGRSQSLSEVLKYEIDVGNESITLG----- 916
DB 1509 LPSTLEVRHNASIRVQTNV--FASKCAENPNSNKS-----FNKLGAEMBSLGKCDPT 1562
QY 917 ---YVNGKLEPLSGYRACVAGFTNITHPONKGLIDGASVSSR--YSDA-VSLP--- 967
DB 1563 QQKCDPPLKPHYVYRISAFVTO-----LFD--EDLKEPTKLYSDTFPSLPTT 1611
QY 968 -QDPGVICGAVFGCIFGALVY---VTVGFIWRRK---RDAKNNEVSFSQIKP----- 1015
DB 1612 ESEP--LFGAIEGVSAQLFLGMLVAVVALLICQKVSNGRERSARLSTRDRPLSVHL 1669
QY 1016 -----KSKLIRVENFEAYFPKQOADSNGFAEYEDLKLVGISQPKYAEIAENRG 1067
DB 1670 NLGQKGRKNTSCPIKINQFEGHFMKLQADSNVYLSKEYBELKOVGRNOSCDIALPENRG 1729
QY 1068 KNRNNVLPYDISRVKLS--VQTHSTDYINANVPGHSHKDFIATQGPLNTLKDTFRM 1126
DB 1730 KNRNNVLPYDATVKSINVDPCSDYINASYIRGNFRREYIVTQGPTEGTDQDFWK 1789
QY 1127 VMEKNVAILIMLTGCVGQRTKCEYWPSSKO--ADQYGDITVAMSEIYLPMTIRDFTVK 1185
DB 1790 VMEQNVNIVNVVQCVKGRKCDHPADDSLYYGLILQMLSESVLPMTIRREFKIC 1849
QY 1186 NIQTSESHPL-ROPHFTSWPDHGVPTDILLINFRVLDVDMKQSPBPSPILVHCSAGV 1244
DB 1850 GEBGLDARLIRHHYVWPDHGVPTTQSLIQVRYVROVYINNSPGAGPFWCSAGVG 1909
QY 1245 RTGFFAIDRLIYOENENTVDYGIYDLRMHRPLMVQTBQVYFLNQCYLDIVRSQKD 1304
DB 1910 RTGFFAIDRLIQLDSDKSDYDIGAVHDRLIRHVMVQTEQYVYLHQCVRDVLRAKL 1969
QY 1305 SKVDLIYQNTAMTYENLAP 1325
DB 1970 RS---EQENPLFPIYENVP 1986
RESULT 11
AD004580
ID AD004580 standard; protein; 1997 AA.
XX
AC AD004580;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human HPTPbeta protein.
XX
KW Protein co-ordinate data; HPTPbeta; HPTP-beta; PTPRB; PTPbeta; PTPB;
KW R-PTP-beta; angiogenesis mediated disorder; diabetic retinopathy;
KW sickle cell anaemia; Paget's disease; mycobacterial infection;
KW systemic lupus erythematosus; myopia; Crohn's disease; psoriasis;
KW rheumatoid arthritis; tumour; acquired immune deficiency syndrome; AIDS;
KW drug designing; therapy; human.
XX
OS Homo sapiens.
XX
PN US2004077065-A1.
XX
PD 22-APR-2004.
XX
PF 04-AUG-2003; 2003US-00634027.

XX 25-SEP-2002; 2002US-0413547P.
 XX (PROC) PROCTER & GAMBLE CO.
 XX PI Evidokimov AG, Pokross ME;
 XX WPI; 2004-374235/35.
 DR N-PSDB; ADO04579.
 DR GENBANK; X54131.
 XX
 PT Identification of compound useful for treatment of angiogenesis mediated
 PT disorder, by using three-dimensional structure of HTPbeta catalytic
 PT domain, and employing structure to design, or select compound that binds
 PT HTPbeta in silico.
 XX
 PS Disclosure; SEQ ID NO 2; 335pp; English.
 XX
 CC The invention relates to the three dimensional coordinates of HTPbeta
 CC (also known as HTP-beta, PTPB, PTPB, PTPB or R-PTP-beta) protein. It
 CC also relates to a method for the identification of a compound useful for
 CC the treatment of an angiogenesis mediated disorder. The compounds
 CC identified by this method are useful to treat diseases like diabetic
 CC retinopathy, sickle cell anaemia, Paget's disease, mycobacterial
 CC infections, systemic lupus erythematosus, myopia, Crohn's disease,
 CC psoriasis, rheumatoid arthritis, solid or blood borne tumours and
 CC acquired immune deficiency syndrome (AIDS). The invention is useful for
 CC the treatment of an angiogenesis mediated disorder or disease. It is also
 CC useful in drug design techniques. The present sequence is human HTPbeta
 CC protein.
 CC
 SQ Sequence 1997 AA;
 Query Match 17.7%; Score 1242; DB 8; Length 1997;
 Best Local Similarity 29.6%; Pred. No. 2.2e-73;
 Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
 QY 123 FPIKAVSISPTVILTWKSNDRASEKVKVAKHKKENKITTIVHQPNCITGLRPAISY 182
 DB 759 FPIKAVSISPTVILTWKSNDRASEKVKVAKHKKENKITTIVHQPNCITGLRPAISY 182
 QY 183 VFSITPGIG--NETWGDPRVYKITEPIVSDLRVALTGVKAAKLSMNGNGTASGRV 238
 DB 797 SVTVTKSGOYVANO--GNGRTI--PEPVKDLTLNRSTEDLHVTWGA-- 844
 QY 239 LIESIGSHE--ELTODSRU-----QVNISDLKRVQY--NINPYLLQSNKT 280
 DB 845 --DVDQYEIQLLFMDKVFPPFHLVMTATEYRFTSLTPRGQYKLVLTISGVQGSFI 901
 QY 281 KG-----DPLG-----TEGLDASN-----TERSRAGSPTAVHDESL 313
 DB 902 EGFVTPSAVKNIHISPNAGTSLTVNMTPGGDDVSYTVAFRHSQKVDSTTIK-- 957
 QY 314 VGPVDPSSGQQRDETEVLLVGLLEPTGRYNATVYQAANGTEGQPALEFRINAIQVDPVT 373
 DB 958 -----VEHTEFHLLEAGEQYQIMIAS--VSGSLAKQINVGRITVPASVQCVI 1002
 QY 374 AVN-ISAISLILIKVSNBESSNVTYKIHVAGETSSNINVSPPRA-----VLPGL 424
 DB 1003 ADNAVSSYSILVSWQKAGVAE--RYDILLTENGILLNRTSPATTKQHKFEDLTPGK 1059
 QY 425 RSTFTYNTVCPVADIEGTGFLQVHPFPVPSDFVTAVSTTEIGLAMSHPDABEFQM 484
 DB 1060 K-----YKQILITVSGGLFSKAQTEGRTPVPAVTDLITENSTHLSFRWTABEGELSWY 1115
 QY 485 HI---TOEGAGNSRVEI--TTNQSIIIGLFPGTKYCEIIVPKGNGTEGASRTVCRTPV 540
 DB 1116 NIFLYNPAGNLOEBAQVDPVLQSPFQNLQGRMYKAVIYTH--SGLSMESIIFGRITVP 1173
 QY 541 SAVDVHVVYVYVTE--WMLDKSPDGASEVYVYHVIKSGKSNSTSTYDAIT--LQGL 596
 DB 1174 ASVSHLGSNRRNTDTSIMFNWSPASGPDF--YELILVNPNGTKEKWKDKDLTEMRFOGL 1232

QY 597 IPGTLYNTISPERVDHWGDPNSTAQYTR-----PSNVSNIDVSTNTTAATL-----SMON 647
 DB 1233 VPGKCYLVAV--VTHSGDLISNKTVAESRTAPSPSILMSFADIANSTLAIWKGPDPWTD 1289
 QY 648 FDDASFTY---SYGLLIEKAGNSSNATQVYDIDITDATYVELIPGSSYVEIFAQYDGG 704
 DB 1290 YNDFELQWLPDALTVEFPYNNKRSBGRITVG-----LPRGRSYQFNVKTVSGDS 1339
 QY 705 IKSL-EPGRKSFCTDPASMASFDEEVVPEKPAVLKWTCPGANAGAELEVSAGANNAT 763
 DB 1340 WKTYSKPIFGSVGRTPKIQWLHCR--PQNSTALICSMIPDSDPDGYSIE-----CR 1390
 QY 764 HLESQSSNGREHYETWYINLF-----STGYNISITVSGGKAAPFRNCTTGIDPP 818
 DB 1391 KMDTQEVESFRKLKEKESLNTIMLVPHKRLVSIKQVSGAMSEVEDSTITMDRPP 1450
 QY 819 PDGSPNI-----TSVSHNSYK--VKESGFEASHPIKAVAVILITG-----EAGHP 862
 DB 1451 P--PPIHRYNEKQDLIKSSINFTVNCWSFSDTNGAVKFTVVRADGSDDELKPEQGP 1508
 QY 863 SADVLKTYDDFKKASDVTYVYIIRTEKGRSQSLSEVLKYEIDVGNSTTLG----- 916
 DB 1509 LPSTLEYRHNASIRVQYTNV--FASKCAENPNSNKS---FNIKLGAEMESLGGKRPD 1562
 QY 917 ---YVNGKLEPIGSRACVAGFTNITFHPQKGLIDGASVYSFR--YSDA--VSLP--- 967
 DB 1563 QQKCDPLKPHRYRSLRAFTQ-----LPD--EDLKEFTPLVSDTFESLPIT 1611
 QY 968 -QDPGVICGAVFGCIFGALVI---VTVGFI FWRKK--RKDAKNNVSPSQIKP----- 1015
 DB 1612 ESEF--LFGAIEGVSAGLFLIGMLVAVVALLICQKVSHGRERPARLSIRDRPLSYHL 1669
 QY 1016 -----KSKKILRVNEFEAFYFKQADNSNGCFABEYEDLKLVGISQPKYAELEANG 1067
 DB 1670 NLGQKGRKTSCTPKINQFGRHFMKLQADSNVLLSKSEYELKDVGNOSCDIALPENN 1729
 QY 1068 KNRNNVLPYDISRVKLS--VQTHSTDYINANMPYHSGKDFIATQGPLPNTLKDFWM 1126
 DB 1730 KNRNNVLPYDARVLYKLSNDDPCSDYINASTIPANNRRREIYVQGLPGTKDDFWKM 1789
 QY 1127 VMEKANYAIIIMLKYCEQGRTKCEBYPSKQ--AQDYGDITVAMTSIVLPEWTRDFTVK 1185
 DB 1790 VMEQVHNIMVYVQCEYKGVKCDHYWPAQDSLYYGDLILQMLSESVLPFWTIRBFKIC 1849
 QY 1186 NIQTESHP--ROFHTSPMDHGVPTDILLNFRVLVADYMKQSPSPSILVHGSAGV 1244
 DB 1850 GEBQDLAHLIRHFTTVPDHSVPEFTQSLIQFRTVADYINRSPGAPFVHCSAGVG 1909
 QY 1245 RTGTFIALDRILYQIENENTVYVGIYDLRMRHPLMVQTEDOYVFLNQCVLDIVRSQKD 1304
 DB 1910 RTGTFIALDRILQQLDSKDSVDIYGAVHDLRLHRYVMVQTECOYVYIHQCVADVLRAR 1969
 QY 1305 SKVDLYQNTMTIYENLAP 1325
 DB 1970 RS---EOENPLPIYENVP 1986
 RESULT 12
 ID AAE20278 standard; protein; 1997 AA.
 XX AAE20278;
 AC AAE20278;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human lung specific gene (LSG) protein #16.
 XX
 KW Human; lung specific gene; LSG; lung embryonic development; cytostatic;
 KW lung cancer; vaccine; gene therapy; non-cancerous lung disease; tumour.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT	Region	145..155
FT	/note= "Antigenic epitope"	
FT	Region	453..465
FT	/note= "Antigenic epitope"	
FT	Region	650..660
FT	/note= "Antigenic epitope"	
FT	Region	714..735
FT	/note= "Antigenic epitope"	
FT	Region	802..823
FT	/note= "Antigenic epitope"	
FT	Region	1040..1062
FT	/note= "Antigenic epitope"	
FT	Region	1121..1132
FT	/note= "Antigenic epitope"	
FT	Region	1281..1295
FT	/note= "Antigenic epitope"	
FT	Region	1307..1318
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FT	Region	1334..1347
FT	/note= "Antigenic epitope"	
FT	Region	1351..1369
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FT	Region	1376..1408
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FT	Region	1532..1545
FT	/note= "Antigenic epitope"	
FT	Region	1644..1655
FT	/note= "Antigenic epitope"	
FT	Region	1671..1681
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FT	/note= "Antigenic epitope"	
FT	Region	1748..1759
FT	/note= "Antigenic epitope"	
FT	Region	1804..1825
FT	/note= "Antigenic epitope"	
FT	Region	1885..1898
FT	/note= "Antigenic epitope"	
FT	Region	1967..1976
FT	/note= "Antigenic epitope"	
XX	WO200208278-A2.	
PN		
XX	31-JAN-2002.	
PD		
XX	20-JUL-2001; 2001WO-US022949.	
PE		
XX	21-JUL-2000; 2000US-0219834P.	
PR		
XX	(DIAD-) DIADEXUS INC.	
PA		
XX	Lung Macina RA, Nair M, Chen S;	
PI		
XX	WPI; 2002-268964/31.	
DR		
XX	Novel lung specific gene useful for identifying, diagnosing, monitoring,	
PT	staging, imaging and treating lung cancer and non-cancerous disease	
PT	states in lung, for gene therapy, and for identifying lung tissue.	
PS	Claim 2; Page 185-192; 197dp; English.	
XX		
CC	The present invention relates to lung specific genes (LSG) and their	
CC	corresponding polypeptides. LSG is useful for identifying, diagnosing,	
CC	monitoring, staging, imaging and treating lung cancer and non-cancerous	
CC	disease states in lung, identifying lung tissue, monitoring and modifying	
CC	lung embryonic development and differentiation, in gene therapy, as	
CC	hybridisation probes), to detect LSG mRNA as a marker for lung cancer, as	
CC	research reagents and materials for discovery of treatments and	
CC	diagnostics to human disease, to detect complementary polynucleotides,	
CC	and/or for chromosome identification. An antibody which binds LSG is useful	
CC	to detect or image localisation of LSG in a patient for detecting or	
CC	diagnosing a disease or condition, for preventing the onset and treatment	
CC	of lung cancer, to isolate or to identify clones expressing LSG	

[illegible]

QY 968 -ODPGVIGCAVFCIGATV---VTYGGIFPWRK---RKDAKNNVESFSQIKP----- 1015
 DB 1612 ESEP--LFGALIEGVASGLFLIGMLVAVVALLICQVSVSGREKSPARKLIRKDRPLSVHL 1669
 QY 1016 -----KSKKILRVENFPAFKKQOADSNCGFAEYEDLKLVGISPKYAAELANNNG 1067
 DB 1670 NIGQKNRKRTKSCPIKNOFGHFMKLOADSNVYLISKEYELKDVGNQSCDIALPENNG 1729
 QY 1068 KKNYNNVLPYDISRVKLS-VQHTSTDYINANMPGYSKQPIANOGGLPMTLDPFWM 1126
 DB 1730 KRRYNNILPYDARVRLSNVDDPCSDYINASTIPGNNFRRETYVQGLPCTKDPFWM 1789
 QY 1127 WEKNVYAIIMLTKEVQGRKCEEYSPSKQ-AQDYGITVAMTSEIVLPENTIRDFYK 1185
 DB 1790 VWEQNNHNIWMVQOCVEKGRVKCDHYMPADQDSLYYGDILQMLSESVALPEMTIREFKIC 1849
 QY 1186 NIQTSRSHL-RQFHTSPDHGVPTTLLINFRIVADYMKQSPSPSPLIVHCSAGVG 1244
 DB 1850 GEGQLDNRHLIRNFHTVMPDHGVPTTSLIQFATVADYINRSBGAPVTVHCSAGVG 1909
 QY 1245 RGTGFLAIDLRLYQLENTVTVGIVYDLRMHRPLAMVQTEQYVFNQCVLDIVRSQKD 1304
 DB 1910 RGTGFLAIDLRLIQGLDSKQSVIYGAVHDLRLHRVHMVQTEQYVFNQCVLDIVRSQKD 1969
 QY 1305 SKVDLIYQNTTAMTYENLAP 1325
 DB 1970 RS-----EENPLPFYENVNP 1986

RESULT 13
 ABR57179
 ID ABR57179 standard; protein; 1997 AA.
 XX ABR57179;
 AC ABR57179;
 DT 02-SEP-2003 (first entry)
 XX
 DE Human PTPRB protein SEQ ID NO:4.
 XX
 XX Tec; protein tyrosine kinase; protein tyrosine phosphatase; PTP10D;
 KM egg derived tyrosine phosphatase; EDRP; antidiabetic; hypotensive;
 KM cardiac; antidiabetic; osteopathic; cytostatic; anorectic; obesity;
 KM immunomodulator; gene therapy; metabolic disease; eating disorder;
 KM body weight regulation disorder; cachexia; diabetes mellitus; cancer;
 KM hypertension; coronary heart disease; hypercholesterolemia; gallstone;
 KM dyslipidaemia; osteoarthritis; sleep apnea; human; chromosome 12;
 KM protein tyrosine phosphatase receptor type B precursor; PTPRB.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO2003047611-A2.
 PN
 XX
 PD 12-JUN-2003.
 XX
 XX 04-DEC-2002; 2002WO-EP013744.
 PF
 XX
 XX 04-DEC-2001; 2001EP-00128844.
 PR
 XX 07-DEC-2001; 2001EP-00129138.
 PR
 XX 02-JAN-2002; 2002EP-00000010.
 XX
 XX (DEVE-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
 PA
 XX
 XX Meise M, Eulenberg K, Fritsch R, Haeder T, Broenner G;
 PI Steuenagel A;
 XX
 XX WPI; 2003-532801/50.
 DR N-PSDB; ACC79776.
 XX
 XX New compositions comprising tyrosine phosphatase PTP10D, protein tyrosine
 PT kinase Tec or egg-derived tyrosine phosphatase genes or proteins, useful
 PT for treating or preventing metabolic diseases, e.g. as obesity or
 PT cachexia.
 XX

PS Claim 2; Fig 8B; 83pp; English.

CC The present invention describes a pharmaceutical composition comprising a
 CC nucleic acid (I) protein tyrosine phosphatase PTP10D, non-receptor
 CC protein tyrosine kinase Tec, egg derived tyrosine phosphatase (EDRP) gene
 CC family or encoded polypeptide, fragment or variant of nucleic acid
 CC molecule or polypeptide, an antibody, an aptamer or receptor recognising
 CC a nucleic acid molecule of PTP10D, Tec, or EDRP gene family or encoded
 CC polypeptide, and a carrier, diluent and/or adjuvant. The pharmaceutical
 CC composition can have antidiabetic, hypotensive, cardiant, antipneumic,
 CC osteopathic, cytostatic, anorectic and immunomodulator activities, and
 CC can be used in gene therapy. The composition is useful for the
 CC manufacture of an agent for detecting and/or verifying, for treating and
 CC alleviating and/or preventing a disorder, including metabolic diseases
 CC such as obesity and other body weight regulation disorders, as well as
 CC related disorders such as eating disorder, cachexia, diabetes mellitus,
 CC hyperextension, coronary heart disease, hypercholesterolemia,
 CC dyslipidaemia, osteoarthritis, gallstones, cancers (cancers of the
 CC reproductive organ), sleep apnea, and other diseases, in cells, cell
 CC masses, organs and/or subjects. The components of the composition may
 CC also be used in controlling the function of a gene and/or gene product
 CC which is influenced and/or modified by a PTP10D, Tec, or EDRP homologous
 CC polypeptide, and for identifying substances capable of interacting with a
 CC PTP10D, Tec, or EDRP homologous polypeptide. The nucleic acid molecule of
 CC PTP10D, Tec, or EDRP family or their fragments, may be used in the
 CC preparation of a non-human animal which over- or under-expresses the
 CC PTP10D, Tec, or EDRP gene product. The present sequence represents human
 CC protein tyrosine phosphatase receptor type B precursor (PTPRB), which is
 CC a human PTP10B homologous sequence. Human PTPRB is located to chromosome
 CC 12
 XX
 XX Sequence 1997 AA;

Query Match 17.7%; Score 1241; DB 7; Length 1997;

Best Local Similarity 29.6%; Pred. No. 2, 6e-73;

Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

QY 123 FDIKAVISPTNYILTMKSNIDTAASEKYVYVHKHMEKNTITVYHQPNINGLRPATSY 182
 DB 759 FDIYETITKRNKFNITQTSIP-----KSENE-----CVFQVLPGRLY 796
 QY 183 VFSITPGIG---NETWGDPRVIVKITEPIVSDLRVALTGVRKALSMNSNGNTASCRV 238
 DB 797 SVTVITKSGQYEANEQ-GNGRTI---DEPVYDLTLRNRSTEDLHVTVSGANG----- 844
 QY 239 LIESISHE-ELTQDSRL-----QVNIISLKGVOY-----NINYYLQSNKT 280
 DB 845 ---DVDQYELQLFNMKVPPPHLVNATERYFTSLPGRQYKTLVLTISGDVQOSAFI 901
 QY 281 KG-----DPLG-----TEGGLDASN-----TERSRAQSPAPVHDESL 313
 DB 902 EGFVPSAVKNIHISPGATDSLIVNMTPGGDVDVSIVTASARHQKQDSQITPHG----- 957
 QY 314 VGVVDSSGQQRDIEVLVIGEPGTRNATVYSGAANGTEGQPAIEFRNAIVFDVT 373
 DB 958 -----VEHTFRLAEAGQYQIMTAS--VSGSLNQJNVVGRTPASVQGVY 1002
 QY 374 AVN-LSATSLTLMKVSNDNESSNTYKIHVAGETDSSNLNVSEPR-----VIRGL 424
 DB 1003 ADNAVSYSYLSWQKAGVAF---RYDILLTEGILLRNSTSEPAITKHKFEDLTPGK 1059
 QY 425 RSTFTYNTVCVGLDIECTPGFLQVHTPPVPSDFRTVTVSTIEGLAMSHDAESFQM 484
 DB 1060 K-----YKIQILTVSGGLFSKEAQGTGRIVPAVVDLTRITENSTRILSPRWASBESLSWY 1115
 QY 485 HI---TOEGAGNSRREI-TTNSIILIGLFEPTKTCCEIIVPKGNGTEGASRTVCNRTVP 540
 DB 1116 NIFLYNPDSNIOERQAVPDLVQSFQNLQGRMYKWIYTH---SGELSNESFIFGRSTP 1173
 QY 541 SAVFDIHVVYVYVTTT-EMLDWKSPPGASEYVYHVIYSKHSNHTSTYDKAIT---LQGL 596
 DB 1174 ASVSHLRGSSNNTTDSLTFMNSPASGDPDF-YELLIVNPNGTKKEMKDKDLTEWRFQGL 1232

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QY 597 IPGLVNTITISPEVDHWGDPNSTAQYTR-----PSNVSNIDVSTNTAATL-----SMON 647
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Db 1233 VPKRKVLAWY---VTHSGDLSNKTASRPAAPSPSLMSFADIANSTLAIWKKPDPMDT 1289
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 648 FDDASPTV---SYCLIEKAGNSNATQVYTDITDATTTELIPGSSVYVEIPAQVGDG 704
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1290 YNDFELOWLPRDALTVFNPYNNRKESEGRIVYG-----LRFGRSYOFNVTVSGDS 1339
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 705 IKSL-EBGRKSFCTDPAASMASPDCEVVPKBPALVAKTCTPGANAGAELEYSASAMNAT 763
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1340 WKYYSKPIFGSVKTPKQIQLHCR-PONSTALACSNIIPDSDDGYSIE-----CR 1390
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 764 HLESCESENGTEYRETYLNF-----STSYNISITVSCGKMAAPRNTCTTGITDPP 818
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1391 KMDTQVEFSPKLEKESLSLNMMLVPHKRYLVSIXVQASGMSEVEVEDSTTMIDRPP 1450
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 819 PDGSPNI-----TSVSHNSVK--VKFSGEASHGPIKAVAVIITG-----EAGHP 862
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1451 P--PPIHRYNKKDVLISKSSINFTVNCWFSPTGAVKFFVYVVRADSGDELKPEQHP 1508
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 863 SADVLTQYDFFKKGASDTVTYVLIIRTEKGRSGLSEVLKYEIDVGNESITLG----- 916
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1509 LPSYLELRHNASIRVYQTNV--FASKCAENPNSNSKS---FNKILAEMESLGGKCDPT 1562
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 917 ---YNGKLEPLGSYRACVAGFTNITFHPONKGLIDGAEYSVFSR--YSDA-VSLP--- 967
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1563 QQKFCGSLPKHTRAYRISIRAFTO-----LFD--EDLKEFTKLYDTPFSLITTT 1611
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QY 968 -QDPGVCIGAVFGCIGALVI---VTVGSPFWKCK--RKDAKNNEVSFSQIKP----- 1015
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QY 1016 -----KSKLIRVNFPAFYPKQOQADNSCGFAEYEDLKIVGISQPKYAEALANRG 1067
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Db 1670 NLQCKGNKRTSCPKIKNQFSGHFMKQADSNLYLSKSEBELKQVGRQSCDIALPENRG 1729
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QY 1127 VMEKNVYAIIMLTVCVQSGTKCEEYWPSPKO-AQDYGDITVAMTSEIVLPEWITRDTVK 1185
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  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1305 SKVDLIYQNTAMTYENTLAP 1325
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Db 1970 RS-----EQENPLFPIYENVNP 1986
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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KM osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
EN W02003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003W0-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW,
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 2135; 180pp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
XX for therapeutic intervention in treating a disease associated with
XX altered mitochondrial function. Specifically, it refers to a method for
XX identifying proteins of the human heart mitochondrial proteome that are
XX useful for drug screening assays, as well as therapeutic targets. The
XX present invention describes a method for identifying such proteins that
XX can be used in the treatment of various diseases associated with altered
XX mitochondrial function including diabetes mellitus, Huntington's disease,
XX osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX compositions have neuroprotective, neurotropic, antidiabetic,
XX anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX cytoskeletal activities. This polypeptide sequence is a human heart
XX mitochondrial protein of the invention.
XX
SQ Sequence 1997 AA;
  Query Match 17.7%; Score 1241; DB 7; Length 1997;
  Best Local Similarity 29.6%; Pred. No. 2.6e-73;
  Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
QY 123 FDIKAVISPTNVILTKSNDTAASEKYVYKHKMEKEKITTVYHQCWNITGRPATSY 182
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 759 FDHYEVLTKKKNKNNFIQTKSIP-----KSENE-----CVFVQLVPRRLY 796
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 VFSITPQIG---NEMTGDPRVIVKITEPIVPSDLRVALGVKRAALSWNGNCTASCORV 238
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 797 SVTVTKSGQYEANEQ-NGRGTI---PEPVKDLTIKRNSTEDLHYWVGANG----- 844
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 LLESIGSHE--ELTQDSRL-----QVNSIDLKPGVQY-----NINPYLQSNKT 280
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 845 ---DVDQYELQLFNDMKVFPFPHLVNTATBYRTSLTPGRQYKILVLITSGDVQQAFTI 901
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 281 KG-----DPLG-----TBGGLDASN-----TERSAAGSPFAVHDESL 313
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 902 EGFTVPFAVKNHISIPGADTSLVNMWTPGSGVDVSTVSAFRUSQVDSQITLPKH----- 957
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QY 314 VGFPDPSSGGQSNDRTEVLVLGLBPGTRYNATVYSGANGTEGQQAIEPTNAIQVEDYT 373
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 958 -----VFETTHRLBNGEYOQIMAS--VSGSLKQOINVAGRTVPASVGCVI 1002
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 374 AVN-ISATSLTLIKVSDNESSNVTYKIHVAGETDSNINVSEPPA-----VTPGL 424
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 1003 ADNAVSYSLVSMOKAGVAB---RYDILLITLNTGILLRNTSEPAATKQHKFEDLTGPK 1059
Qy 425 RSSTFYNTITCPVLADIEGTPGLQVTPVPVSDRYVTVSTTELGAMSSHDESRQM 484
Db 1060 K-----YKIQILTVSGGLFSKKAQTEGRTVPAVATDITLNTENSTRHSFEFWTSEBELSMY 1115
Qy 485 HI---TOEGAGNSRVEI--TTNOSIIIGLFPGRKYCFEIVPQPGNTEGASRTVCNRTVP 540
Db 1116 NIFLYPNPDNLQERAVDPLVQSFQNLQGRMYKVIIVTH--SGELSNSEFIRGRYVP 1173
Qy 541 SAVFDHVVVYVTTTE--MMDWKSPPGASVYVHLVYESKGSNHTSTYDKAIT---LQGL 596
Db 1174 ASVSHLRGSRNNTTSLMFMNMSPDAGDFP--YELLVYNGNGTKKNWKKDITLWRFQGL 1232
Qy 597 IGTLLVNTTISPEVDHVMGDPNSTAQYTR-----PSNVSNIVSTNTTAATL---SMON 647
Db 1233 VPGKRVLMV-----VTHSGDLNKKVTAESTTASPPSLMSFADIANTSLAITKGPDPWTD 1289
Qy 648 FDDASPTT---SYCLIIIEKAGNSNATQVYVDIGITDATTLELPGSSYVTEIFAQVGDG 704
Db 1290 YNDFELQMLPRDALTVFNPYNNRKSREGRIYVG-----LRGRSYQFNVKTVSGDS 1339
Qy 705 IKSJ--EPGRKSPCTDPASASFDCEVVPREPALVLTCTCPREANAGFELEVSQGANAT 763
Db 1340 WKTYSKPIFGSVTRKPDKIQLHCR--PONSTAIACSWIPPSDFDGYSE-----CR 1390
Qy 764 HLESCSSENGTEYRTEVYVLPN-----STSYNISITTVSCGMMAPTNTCTGTIDPP 818
Db 1391 KMDTQEVERFSRKLKEKSLNIMLMVPHKRYLVSIKVQASGMTSVSDSTITMIDRPP 1450
Qy 819 PDGSPNI-----TSVSNYSVK--VKESGFASHPPIAVAVILTTG-----EAGHP 862
Db 1451 P--PHHIVNEKDVILSKSSINFTVNCMFDPMNAVYFTVVRREADGSDLEKPEQHP 1508
Qy 863 SADVLKTYTDDFKKASDPTVYTLIRTEKRSOSLSVLYKXEDVGNSTTG----- 916
Db 1509 LPSYLEYHNHNASIRYQYNY--FASKCAENPNNSKS-----FNKLGAMSLGCKDPT 1562
Qy 917 ---YVNGLELPGLGYRACVAGFTNTTFRPQNKGLDGAESYVSFSR--YSDA-VSLP--- 967
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Qy 968 -QDPGVICGAVFGCFFGLVLT---VTYGGFIFMRKK---RDAKANEVSPQIRP----- 1015
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Qy 1068 KNRNNTVLPYDISVKYS--VQHTSTDYINANWPGYHSHKKDITATQGLPNTLKDFWM 1126
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Qy 1127 VMEKNVVAIIMLTGCEQGRKCEYWPSSKO--ADQYGDITVAMTSELYLEBMTIRDPYVK 1185
Db 1790 VMEQNVNIVWVTCVEKGRKCHMYPAODDSLTYGBLLQMLSSVLEBMTIREKTKC 1849
Qy 1186 NITQSESHPL--RQHTTSWPDHGVDTTDLINERKLVDRYMKQSPPEPILVHCSAGVG 1244
Db 1850 GEEOLDHRLRHRHRYHTWPDHGVETQSLIGFRVTRDYINRSPAGPTVHCAGVG 1909
Qy 1245 RTGFEIADILLYOENENVDVYGYUDDLRMRPLMVQTEODVYFNQCVLDIVSOKD 1304
Db 1910 RTGFEIADILRLOQDSDVDYIGAVHDLRLRVRHVWQTECOYVYLHQCVRDVLARKL 1969
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Db 1970 RS-----EQENPLPEIYENVNP 1986

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RESULT 15
AAM79805

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ID AAM79805 standard; protein; 2002 AA.
XX AC AAM79805;
XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 3451.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX OS Homo sapiens.
XX MN MO200157190-A2.
XX PD 09-AUG-2001.
XX PF 05-FEB-2001; 2001MO-US004098.
XX PR 03-FEB-2000; 2000US-00496914.
XX PR 27-APR-2000; 2000US-00560875.
XX PR 20-JUN-2000; 2000US-00598075.
XX PR 19-JUL-2000; 2000US-00620325.
XX PR 01-SEP-2000; 2000US-00654936.
XX PR 15-SEP-2000; 2000US-00663561.
XX PR 20-OCT-2000; 2000US-00693325.
XX PR 30-NOV-2000; 2000US-00728422.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,
PI Xue AJ, Yang Y, Wejrtman T, Goodrich R,
XX DR WPI; 2001-476283/51.
XX DR N-PSDB; AAK52938.
XX PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX PS Claim 20; Page 340-341; 6221pp; English.
XX XS The invention relates to polynucleotides (AAK51456-AAK51435) and the
XX encoded polypeptides (AAM78923-AAK80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibitin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication.
SQ Sequence 2002 AA;
Query Match 17.7%; Score 1241; DB 4; Length 2002;
Best Local Similarity 29.6%; Pred. No. 2,6e-73;
Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;
Qy 123 FDIKAVSISPTVNLITWKSNTTAASEYKVVYKHKNENKITTIVHQPNCNITGLRPATSY 182
Db 764 FDHYEVITIKANNPQYTSIP-----KSENE-----CYFVQVLPGLY 801
Qy 183 VFSITPGIG---NETWGDPRVIVKITEPIVPSDLRVALTGVRAALSWNSNGTASCNV 238
Db 802 SVTVTTKSGQYEANBQ--GNGRTI-----PEPVKDLTLRNSTEDLHTWGSANG----- 849
Qy 239 LLESTGSHE--ELTQDSRL-----QVNISDLKPGVQY-----NINPYLLQSNKT 280

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:57:02 ; Search time 46 Seconds
(without alignments)
2169.691 Million cell updates/sec

Title: US-09-516-728A-4

Perfect score: 7030
Sequence: 1 MKPAAEARLPSPSGIRMA.....TIYENLAPYTFKNGYIA 1337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6824	97.1	1337	3	US-08-854-585-2
2	6824	97.1	1337	4	US-09-447-533-2
3	6824	97.1	1337	5	PCT-US95-05512-2
4	1242	17.7	1997	4	US-09-949-016-6275
5	1241	17.7	1903	4	US-09-949-016-8049
6	954	13.6	1711	2	US-08-342-930-2
7	864	12.3	2301	4	US-09-822-871-4
8	855	12.2	1188	1	US-08-201-697-4
9	854	12.1	1246	4	US-09-949-016-8051
10	854	12.1	1246	4	US-09-949-016-8052
11	854	12.1	1246	4	US-09-949-016-8053
12	854	12.1	1246	4	US-09-949-016-8054
13	854	12.1	1246	4	US-09-949-016-8055
14	842	12.0	1187	1	US-08-201-697-2
15	841	12.0	1274	4	US-09-949-016-8828
16	841	12.0	1274	4	US-09-949-016-8829
17	841	12.0	1274	4	US-09-949-016-8830
18	841	12.0	1274	4	US-09-949-016-8831
19	841	12.0	1274	4	US-09-949-016-8832
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22	815.5	11.6	1911	1	US-08-348-006B-5
23	815.5	11.6	1911	2	US-08-800-825A-5
24	815.5	11.6	1911	3	US-09-158-657-5
25	815.5	11.6	1911	5	PCT-US94-10166-5
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27	785.5	11.2	1452	2	US-08-991-258A-4

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29	785.5	11.2	1452	3	US-08-991-953A-4	Sequence 4, Appli
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31	778.5	11.1	254	2	US-09-144-925-14	Sequence 14, Appli
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34	748	10.6	898	1	US-08-036-210-22	Sequence 22, Appli
35	748	10.6	898	1	US-08-449-609-22	Sequence 22, Appli
36	748	10.6	898	4	US-09-361-096A-22	Sequence 22, Appli
37	742.5	10.6	1501	2	US-08-447-464-3	Sequence 3, Appli
38	742.5	10.6	1501	2	US-08-716-679-3	Sequence 3, Appli
39	737.5	10.5	506	4	US-09-949-016-8833	Sequence 8833, Ap
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41	737.5	10.5	506	4	US-09-949-016-8835	Sequence 8835, Ap
42	737.5	10.5	506	4	US-09-949-016-8836	Sequence 8836, Ap
43	737.5	10.5	506	4	US-09-949-016-8837	Sequence 8837, Ap
44	737.5	10.5	506	4	US-09-949-016-8838	Sequence 8838, Ap
45	720.5	10.2	1075	4	US-09-949-016-8308	Sequence 8308, Ap

ALIGNMENTS

RESULT 1
US-08-854-585-2
Sequence 2, Appli US/08854585
Patent No. 6114140
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and Stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/237,940
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-585-2
Query Match 97.1%; Score 6824; DB 3; Length 1337;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;
QY 1 MKPAAEARLPSPSGIRMAPIIIILRLICQILICAGTSPSPDPSPVAVATGNGITQ 60
Db 1 MKPAAEARLPSPSGIRMAPIIIILRLIRGQILICAGTSPSPDPSPVAVATGNGITQ 60
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Db      361  ERTNAIQVFDVTAVANISATSLTLTWKSDNESSSNVYTKIHAGETDSNINVEPRAY 420
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Db      1321  ENLAPVTFGKTNGYIA 1337

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RESULT 2
US-09-447-533-2
; Sequence 2, Application US/09447533
; Patent No. 6552169
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K.
Oeltnan, Arne
TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
PHOSPHATASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed IP Law Group PLLC
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/447,533
FILING DATE: 23-No. 6552169-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Roseman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 200125.402C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-447-533-2

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Best Local Similarity 97.4%; Pred. No. 0;
Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;
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DB 361 EFTNAIQVFDVAVNISATSLTLIMKVSNDNESSNTYKIHVAGETDSSNLANSERPAV 420
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DB 601 LYNITISPEVDHVGDNPSIAQYTRPSNVSNIDVSTNTAATLSQWNPDDASPTYSYCLL 660
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DB 721 SMASFDDEVVPEKRALVAKTCTCPGANAGFLEVSAGANNATLHESCSSNGTEYRTV 780
QY 781 TYLNFTSTYNIISITTVSCGMAAPTRNTCTTGITDPPDDSPNITSVSHNSVVKFSGF 840
DB 781 TYLNFTSTYNIISITTVSCGMAAPTRNTCTTGITDPPDDSPNITSVSHNSVVKFSGF 840
QY 841 EASHGPIKAYAVILITTEBAGHPADVLYTYDDPKKASDITYTYLLIRTEKGRSQSLSE 900
DB 841 EASHGPIKAYAVILITTEBAGHPADVLYTYDDPKKASDITYTYLLIRTEKGRSQSLSE 900
QY 901 VLKKEIDVGNESFTLGYYNGKLEPLGSRACVAGFTNITTFHPQKGLIDGASIVSFSRY 960
DB 901 VLKKEIDVGNESFTLGYYNGKLEPLGSRACVAGFTNITTFHPQKGLIDGASIVSFSRY 960
QY 961 SDAVSLPQDQGVLCGAVFGCIFGALVITVVGFI FWRKKRKAONNEVSFSQIKPKSKL 1020
DB 961 SDAVSLPQDQGVLCGAVFGCIFGALVITVVGFI FWRKKRKAONNEVSFSQIKPKSKL 1020
QY 1021 IRVENFAIRFKKQADSNCGAEBEYEDLKVGISQPKYAAELAKNGKNYNNVLPDIS 1080
DB 1021 IRVENFAIRFKKQADSNCGAEBEYEDLKVGISQPKYAAELAKNGKNYNNVLPDIS 1080
QY 1081 RYKLSVQTHSTDDYINANNYMGYSKKOFITAGPLPNTLKDPRMWEKKNVYAILMLTK 1140
DB 1081 RYKLSVQTHSTDDYINANNYMGYSKKOFITAGPLPNTLKDPRMWEKKNVYAILMLTK 1140
QY 1141 CVBQGRTRCEBYWPSKQADYDITVAMTSEI VLPWTIRDPYKNIQTSESHPLRQHF 1200
DB 1141 CVBQGRTRCEBYWPSKQADYDITVAMTSEI VLPWTIRDPYKNIQTSESHPLRQHF 1200
QY 1201 TSWPDHGVPTDILLINFRILYVRDYMKQSPESPILVHCSAGVGRGFIADILLIYQIE 1260
DB 1201 TSWPDHGVPTDILLINFRILYVRDYMKQSPESPILVHCSAGVGRGFIADILLIYQIE 1260
QY 1261 NENTVDYGYIYDLMRMRPLMWQTEQVFLNQCVLDIRSQKSKVDLLIYQNTTAMTIY 1320

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DB 1261 NENTVDYGYIYDLMRMRPLMWQTEQVFLNQCVLDIRSQKSKVDLLIYQNTTAMTIY 1320
QY 1321 ENLAPVTTFGKNGXYIA 1337
DB 1321 ENLAPVTTFGKNGXYIA 1337

RESULT 3
PCT-US95-05512-2
: Sequence 2, Application PC/TUS9505512
: GENERAL INFORMATION:
: APPLICANT: Tonks, Nicholas K. and stman, Arne
: TITLE OF INVENTION: Density Enhanced Protein Tyrosine
: TITLE OF INVENTION: Phosphatase
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Borun
: STREET: 233 South Wacker Drive, Suite 6300
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/05512
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Borun, Michael P.
: REGISTRATION NUMBER: 25,447
: REFERENCE/DOCKET NUMBER: 27866/31954
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1337 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-05512-2

Query Match 97.1%; Score 6824; DB 5; Length 1337;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;

QY 1 MKPAAERARLPSPSGRLMALPLILLRLGQILCAGTSPPIPDPSVATVATENGITQ 60
DB 1 MKPAAERARLPSPSGRLMALPLILLRLGQILCAGTSPPIPDPSVATVATENGITQ 60
QY 61 ISSAESFHKONGTGOVETNTSDESSGANDSLRTPREGSNGTGAOKTSPSTGPS 120
DB 61 ISSAESFHKONGTGOVETNTSDESSGANDSLRTPREGSNGTGAOKTSPSTGPS 120
QY 121 PVFDIKAVSISPTNVILTWKSNDDTAASEYKVVYGHKMEKNTITVYHQPCNITGLBPAT 180
DB 121 PVFDIKAVSISPTNVILTWKSNDDTAASEYKVVYGHKMEKNTITVYHQPCNITGLBPAT 180
QY 181 SYFSTIRPGIGNETWGDPRVIAKVTBEPVSDLRVALTVGRKALSNNGNGTASCRVLL 240
DB 181 SYFSTIRPGIGNETWGDPRVIAKVTBEPVSDLRVALTVGRKALSNNGNGTASCRVLL 240
QY 241 ESIGSHELTQDSRLQVNIISDLKPGVOYNINPYLLQSNKTKGDPGLTEGGGLDASNTSR 300
DB 241 ESIGSHELTQDSRLQVNIISDLKPGVOYNINPYLLQSNKTKGDPGLTEGGGLDASNTSR 300
QY 301 AGSPPTAVHDESLVGPVDPSSGQSDRTEVLLVGLBEGTRNATNAVYSQAANGTEGQPOAI 360
DB 301 AGSPPTAVHDESLVGPVDPSSGQSDRTEVLLVGLBEGTRNATNAVYSQAANGTEGQPOAI 360

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Db 301 QGAPPLCMNSPFVGVDPSSGOOSRDETVLVLGEPGTRYNATVYSQANGTEGQPAI 360
 QY 361 EFRTNALQVEDYAVANISATSLTLIMKVSNDNESSNVTYKIHAGSTDSNINVSPPAV 420
 Db 361 EFRTNALQVEDYAVANISATSLTLIMKVSNDNESSNVTYKIHAGSTDSNINVSPPAV 420
 QY 421 IPELRSTFNITVCVPLGDIESTPGFLOVHPVPVSDPRVTVSTTEIGLWASHDAE 480
 Db 421 IPELRSTFNITVCVPLGDIESTPGFLOVHPVPVSDPRVTVSTTEIGLWASHDAE 480
 QY 481 SFQMHITQEGAGSRVEITTNOSIIIGLPGTKCFEIVPGPMTGASRTVCNRYTP 540
 Db 481 SFQMHITQEGAGSRVEITTNOSIIIGLPGTKCFEIVPGPMTGASRTVCNRYTP 540
 QY 541 SAVFDIHVVYVTTTMMLDKSPDGASEYVHLVIESKGSNHTSTYDKAITLQGLIPGT 600
 Db 541 SAVFDIHVVYVTTTMMLDKSPDGASEYVHLVIESKGSNHTSTYDKAITLQGLIPGT 600
 QY 601 LKNTITSEVDHWGDPNSTAQTTPSNVSNIDVSTNTTAAATLSMONEPDASPTYSYCL 660
 Db 601 LKNTITSEVDHWGDPNSTAQTTPSNVSNIDVSTNTTAAATLSMONEPDASPTYSYCL 660
 QY 661 IEKAGNSNATQVVDIGITDAITVELIPGSSYTBEPVOVDGKSLERGRKSCTPA 720
 Db 661 IEKAGNSNATQVVDIGITDAITVELIPGSSYTBEPVOVDGKSLERGRKSCTPA 720
 QY 721 SMASFDCEVVPKEPALVILKMTCPPGANAGFELEVSSGAMNNATHESSSENGTEYRETV 780
 Db 721 SMASFDCEVVPKEPALVILKMTCPPGANAGFELEVSSGAMNNATHESSSENGTEYRETV 780
 QY 781 TLANSTSTNITITVSCGKMAAPTRNTCTTGTITPPPDGSPNITSVSHSVKXSGF 840
 Db 781 TLANSTSTNITITVSCGKMAAPTRNTCTTGTITPPPDGSPNITSVSHSVKXSGF 840
 QY 841 EASHGPRIKAYAVILITTEGAGHPSADVILKTYDDFKKAGSDTYVTLITTEKGRSOSISE 900
 Db 841 EASHGPRIKAYAVILITTEGAGHPSADVILKTYDDFKKAGSDTYVTLITTEKGRSOSISE 900
 QY 901 VLKXEDIVGNESSTLGYNGKLEPLGSTRACVAGFTNTTTPHONKGLDGAESYVSFGRY 960
 Db 901 VLKXEDIVGNESSTLGYNGKLEPLGSTRACVAGFTNTTTPHONKGLDGAESYVSFGRY 960
 QY 961 SDAVSLPODPGVICGAVFGCITFGALVITVGGFTFMRKKRDANKNEVSFOIIPKSKL 1020
 Db 961 SDAVSLPODPGVICGAVFGCITFGALVITVGGFTFMRKKRDANKNEVSFOIIPKSKL 1020
 QY 1021 IRVENFEAYFKKQOQADSNCGFAEEYEDLKVGISQPKYAEIAENRGKRNRYNNVLPYDIS 1080
 Db 1021 IRVENFEAYFKKQOQADSNCGFAEEYEDLKVGISQPKYAEIAENRGKRNRYNNVLPYDIS 1080
 QY 1081 RYKLSVOCHSTDDYTNANMYMGYHSKOPFATQGPLPNTLKDFFRMWKKVAVAILMLTK 1140
 Db 1081 RYKLSVOCHSTDDYTNANMYMGYHSKOPFATQGPLPNTLKDFFRMWKKVAVAILMLTK 1140
 QY 1141 CVEGRTKCEBYWPSKQADYGDITVAMTSEIVPEWTIRDFYKNIQTSSEHPLRQFHF 1200
 Db 1141 CVEGRTKCEBYWPSKQADYGDITVAMTSEIVPEWTIRDFYKNIQTSSEHPLRQFHF 1200
 QY 1201 TSWPDHGVPTDITLLINFRYIVRDYMQSPESPILVHCSAGVGRSTFIALDRLIYOIE 1260
 Db 1201 TSWPDHGVPTDITLLINFRYIVRDYMQSPESPILVHCSAGVGRSTFIALDRLIYOIE 1260
 QY 1261 NENIVDYGIYVYDLMRHRPLVOTEDQVFLNQCVLIVSOKDSKDLIYONTAMTIT 1320
 Db 1261 NENIVDYGIYVYDLMRHRPLVOTEDQVFLNQCVLIVSOKDSKDLIYONTAMTIT 1320
 QY 1321 ENLAPVTTFGKTINGYIA 1337
 Db 1321 ENLAPVTTFGKTINGYIA 1337

; Sequence 6275, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C1001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6275
 ; LENGTH: 1997
 ; TYPE: PR1
 ; ORGANISM: Human
 ; US-09-949-016-6275

Query Match 17.7%; Score 1242; DB 4; Length 1997;

Best Local Similarity 29.6%; Pred. No. 2,7e-71;

Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

QY 123 FDIKAVISSTPNVILTKSNDTASERYVYKHKMENKTTIVVHOPMCNITGLRPATSY 182
 Db 759 FDHVEVITKKNFIFQTKSLP-----KSHNE-----CVFVQLVGRILY 796
 QY 183 VFSITPGIG---NEWGDPRIKIVTEPIVSDLEVALTGVRKALMSNGNGTSCV 238
 Db 797 SVTVTTKSGOYEANEQ-GNKRITL-----BEVYKDLTKRSTEDLHVTSANG----- 844
 QY 239 LLSISGSH-ELTQDSRL-----QVNISDLKGVQY-----NINPYLLQSNKT 280
 Db 845 ---DVDQYELQLLFNMKVFPPFHLVNTATEYRFTSLTGRQYKILVLTISGVOQSART 901
 QY 281 KG-----DPLG-----TEGGIDASN-----TERSRASPPAPNHDESL 313
 Db 902 EGFVTSAYKNIHISNNGATDLSLTWNTPGGQDVDSVTVSAPRHSQKXDSQITPKH---- 957
 QY 314 VGPVDSGOOSRDETVLVLGEPGTRYNATVYSQANGTEGQPAIEFRTNALQVFDVT 373
 Db 958 -----VFEHTFRLBAGRQYQIMLAS--VSSGLKQCNVGVRTVPAVQGYI 1002
 QY 374 AVN-ISAATSLTLIMKVSNDNESSNVTYKIHVAGETDSNINVSPPA-----VITGL 424
 Db 1003 ADNAVSSYSLIVSWOKAGVAB--RYDILLITENGILLRNTSEPAITTKQHKFEDLTGK 1059
 QY 425 RSSTFYNTVCVPLGDIESTPGFLOVHPVPVSDPRVTVSTTEIGLWASHDAESQ 484
 Db 1060 K-----YKIOIILVSGGLPESKEQTEGRVPAAVTLRLTENSIRHLSFRWTASBESLSWY 1115
 QY 485 HI---TOEGAGNSRVEI--TTNOSIIIGLFPGTKYCFEIVPGPMTGASRTVCNRYTP 540
 Db 1116 NIFLYNPQDNLQERAOVPLVQSFQONLQGRMTKMIIVTH--SGELSNSFIFGRIVP 1173
 QY 541 SAVFDIHVVYVTTTMMLDKSPDGASEYVHLVIESKGSNHTSTYDKAITLQGLIPGT 600
 Db 1174 ASVSHLRGSNNTTDSLTFMNSPASGDFD-YELLVYNPQGTCKENMXDKULTWRPFGGL 1232
 QY 597 IEGTLNITISPEVDHWGDPNSTAQTTPSNVSNIDVSTNTTAAATLSMONEPDASPTYSYCL 660
 Db 1233 VPGKRYLVW---VHSGDLSNKVTAESRTAPSPSLSMSPADIANATSLATLWKGPDPWTD 1289
 QY 648 FDDASPTT---SYCLLEKAGNSNATQVVDIGITDAITVELIPGSSYTBEPVOVDGKSLERGRKSCTPA 720
 Db 1290 YNDFEIQMLPRDALVFNPNYNNRKEGRIVG-----LBPGRSYQFNVATVSGDS 1339
 QY 705 IKSL-EPGRKSCFCTDPASMAFDCVVPKEPALVILKMTCPPGANAGFELEVSSGAMNNAT 763

RESULT 4

US-09-949-016-6275

```

Db      1340 WKTYSKEIFGSRVTRKPKDKIOMLHCR-PONSTAIACSWIPDSDPDGYISB-----CR 1390
Qy      764 HLESCESENGREYRETEVYTLNF-----STSYNISITTVSCGKMAAPRNRTCTGTIDPPP 818
Db      1391 KMDTOEVEFSRKLKEKESLSLIMMLVPHKRLVSIKQOSAGMTSEVEDSTTTMIDRPP 1450
Qy      819 PDGSPNI-----TSVSHNSVK--VKFSGFASHGPIKAVAVILTTG-----EAGHP 862
Db      1451 P-PPHIRVNEKODVLISKSGINFTVNCWSPDNTGAVKFFTVVVRADGDELKPEQHP 1508
Qy      863 SADVLKTTYDDFKKASDITYTYLIRTEBKRSQSLSEVLKYEIDVNGESTTLC----- 916
Db      1509 LPSYLEFRHNASIRVQOTNY--FASKCAENPNSNKS----FNIKLGAEMESLIGKXDP 1562
Qy      917 ---YUNGKLEPLGSRACVAGFTNITFHPOKGLIDGASVVSFR--YSDA-VSLP--- 967
Db      1563 QQKFCDBPLKPHYRISIRAFTO-----LPD--EDLKEFTKPLSDTFFSLPTT 1611
Qy      968 -ODPGVIGAVFGCIFGALVI--VTVGFIWRRK--RKDAKNEVSFSQIKP----- 1015
Db      1612 ESEP--LFGAIEGVSAGLPLIGMLVAVALLICQKXSHGERPSARLSIRDRPLSVHL 1669
Qy      1016 -----KSKLIRVENFEAYFKQOQADNSCGFAEYEDLKVIGISQPKYAAELANRG 1067
Db      1670 NLGQGNRKRTSCPIKIQFEGHFMKLQADSNVLLSKEYEELKDVGRQSCDIALPENRG 1729
Qy      1068 KNRYNVNLPRDISVKLS-VQTHSTDDYINANWAGYHKKDFIATQGLPNTLKDFRM 1126
Db      1730 KNRNNNLPRDARKVKSNDDBPCSDYINASYIPGNFRREYLVTOGLGTQDDWPKM 1789
Qy      1127 VWEKNVAIIMLTKVEQGRKCEEYWPSSKO-AQYGDITVAATSEIYLPMTIRDPYVK 1185
Db      1790 VMGNVNIIMVWQCVKGRKCDHWPAODDSLYGDLILQMLSESVLPMTIRREKIC 1849
Qy      1186 NIGTSEHPL-ROFHTSPDHGVPDITDLINFRYLVRDYMKSPSPSPLVHCSAGVG 1244
Db      1850 GEBQDLHRLIRHRYHWMPDHGVPEETQSLIQFRTVRDYINRSPAGPFTVHCSAGVG 1909
Qy      1245 RTGFTIADILYIOEENYVYGIYVDLRMRPLWQTEDOYVPLNQCTDLVRSQKD 1304
Db      1910 RTGFTIADILYIOEENYVYGIYVDLRMRPLWQTEDOYVPLNQCTDLVRSQKD 1969
Qy      1305 SKVDLYIQTMTATYENLAP 1325
Db      1970 RS-----EQENPLFIYENVNP 1986

RESULT 5
US-09-949-016-8049
; Sequence 8049, Application us/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8049
; LENGTH: 1903
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8049
Query Match      17.7%; Score 1241; DB 4; Length 1903;

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Best Local Similarity 29.3%; Pred. No. 2,96-71;
Matches 395; Conservative 198; Mismatches 507; Indels 248; Gaps 54;

Qy      125 IKASISPT-----NVILTWKSNDRFASEYKVVH-----KNEENKITIVHQ 169
Db      646 VQGVSVNSASRSDYLRAVSWHATGDPHYETVITLKNKNFIQTSKIPSENE----- 696
Qy      170 WCNIITGLRPATSYVFSITPGIG-----NETWGDPRVIVKITEPIVPSDLRVALTGVRKAL 225
Db      697 -CVFQVLPGRLVYVYTTTSGQYEANQ--GNGGTI-----PEVYKOLLTLNRSTEDLHV 749
Qy      226 SMSNGNGTASCRVLLESIGSHE--ELTQDSRL-----QVNISDLKPGVQY----- 268
Db      750 TWSGANG-----DVDQYEIQLFNMDKVPFPHLVNTATREFTSLTRGQYKLV 800
Qy      269 -NINPYLQSNKYG-----DPLG-----TEGGLDASN-----TERSR 300
Db      801 LTTISGDVQOQSAFIEGFTVPSAVKNHISPGCATDSLTVNMTPGGGDVDSYTVSAFRHSQK 860
Qy      301 AGSPFAPVHDSLVGVPDPSGQQRDTEVLLVGLRGTRYNATVYSOAANGTEGQPOAI 360
Db      861 VDSQTIIRK-----VFERTFHLLEAGEQYQIMIAS--VSGSLKQNLNV 901
Qy      361 EFRNIAIQVDPVTAVN-ISAISLTLIKVSDNESSNVTYKIHVAGETDSSNLVSEPR 419
Db      902 VGRTPASVQGVLIADNAVSSYSLIVSWOKAGVAE---RYDILLTEGILLRMTSEPAT 958
Qy      420 -----VIRGLASSFFNYITVCPVIGDIEGTGFIQVHPRPVPSDFRTVSTTEIG 471
Db      959 TKQHFEDLTPGKK-----YKIQILTVSGGLFSKSAQTEGRVPAVVDLRTENSTRLS 1014
Qy      472 LWSHSHAESFQMI---TOGAGNSRVEI--TTQSLIIGGLPQTKYCFEIVPKPGNCT 527
Db      1015 FRMTASEGLSWYIFILNPENGLQERAOVDPLVQSSFOQLGRMYKMYIVH--SGE 1072
Qy      528 EGASRTVCNRTVPSAVPDIHVVYTTTE--MWLDKSPDGASEYYHLVIESKHGNSHTST 586
Db      1073 LSNESFIFGRVTPASVSHLRGNSRNTTDSLWFNNSPASGPDF--YELLVYNPGTKKENW 1131
Qy      587 YDKAIT---LQGLIRGLNITISPEVDHVGDNSTAOYTR-----PSNNSNIDVSTNT 638
Db      1132 KDKDLTEMRFGVLPGKRYVLMV---VTHSGDLSNKYTAESRTAPSPSLMSFADIANTS 1188
Qy      639 TAATL-----SWQNDPASPTV---SYCLILEKAGNSSNATOVVDIGITATVTELI 691
Db      1189 LAITWKGPBDWTIDNDELQELPRDALTVFPYNNKRSSEGRIVG-----LRGR 1238
Qy      692 SYTVEIFAQVGDGKSL-EPGRKSFCTDPASMASPDECVVPKEBALVLMKCPGANAGF 750
Db      1239 SYQFNVTVSGDSMKTVSKPIFGSVTRTKPIQMLHCR-PONSTAIACSWIPDSDPDGY 1297
Qy      751 ELEVSAGMNNATHLBSCSSENGTEYRETYTLNF-----STSYNISITTVSCGMAAPT 805
Db      1298 SIE-----CRMDQVEFEFSRKLKEKESLSLIMMLVPHKRLVSIKQOSAGMTSEV 1349
Qy      806 RNTCTGTIDPPRPGSPNI-----TSVSHNSVK--VKFSGFASHGPIKAVAVILTTG 857
Db      1350 EDSITTMIDRPPP--PPHIRVNEKVDLISGGINFTVNCWSPDNTGAVKFFTVVVRAD 1407
Qy      858 -----EAGHPADVLKTYDDFKKASDITYTYLIRTEBKRSQSLSEVLKYEIDVG 909
Db      1408 DGDDELKPEQHPPLPSYLEFRHNASIRVQOTNY--FASKCAENPNSNKS----FNIKLG 1461
Qy      910 NESTTLC-----YUNGKLEPLGSRACVAGFTNITFHPOKGLIDGASVVSFR-- 959
Db      1462 AEMESLQKCDPTQOKCDBPLKPHYRISIRAFTO-----LPD--EDLKEFTKPL 1510
Qy      960 -YSDA-VSLP---QDPGVIGAVFGCIFGALVI--VTVGFIWRRK--RKDAKNE 1007
Db      1511 LYSDFPSLPTTTSER--LFGAIEGVSAGLPLIGMLVAVALLICQKXSHGERPSAR 1568
Qy      1008 VFSQIKPKSKL-----IRVENFEAYFKQOQADNSCGFAEYEDLKVIGISQPKYAA 1060

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Db 1569 LSIIRDRLPSVHLNLGQKPIKINQFEGHFMKLQADSNYILSKEYBELKDVRGNQSCDIA 1628
 QY 1061 ELAENKGRKRNUNVLYDYDSRYVLS-VQHSRDDYNNANMPGYSKDFATQGPPLNT 1119
 Db 1629 LIPENKGRKRNUNVLYDYDSRYVLS-VQHSRDDYNNANMPGYSKDFATQGPPLNT 1688
 QY 1120 LNDPFWMEKVNVALIMLTKECQGRKCEWYSPSKQ-AQDYGDITVMTSEIYLPENT 1178
 Db 1689 KQDFMFWMEQVNHVIMVLTQCEKGRVACDHVMPADQSLYGGDILLOMLSESVLPENT 1748
 QY 1179 IADFTYKNIQTSSEHPL-RQHFHTSPWPDIGVDPDTDLINFRYLVADYKQSPSPPLIV 1237
 Db 1749 IBEFKICGSEQLDAHRLHFRHYTWPDHGVPEITQSLIOFVRTVADYINRSFGAGPTVV 1808
 QY 1238 HCSAGVGRGTFTALDRILYQIENENTVDVGVYVLDLHMRPLMVTQEDQVYELMQCYLD 1297
 Db 1809 HCSAGVGRGTFTALDRILYQIENENTVDVGVYVLDLHMRPLMVTQEDQVYELMQCYLD 1868
 QY 1298 IYRSQKDSKVLDLIYQNTTAMTYENLAP 1325
 Db 1869 VLRARKLRS---EQENPLFPYENVNP 1892

RESULT 6
 US-08-342-930-2
 / Sequence 2, Application US/08342930
 / Patent No. 5821084
 / GENERAL INFORMATION:
 / APPLICANT: OLMSTED, ELIZABETH A.
 / APPLICANT: MAURO, LAURA J.
 / APPLICANT: DIXON, JACK E.
 / APPLICANT: TITILE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
 / TITLE OF INVENTION: PHOSPHATASE
 / NUMBER OF SEQUENCES: 13
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: MORRISON & ROEBSTER
 / STREET: 755 Page Mill Road
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94304-1018
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/342,930
 / FILING DATE: 21-NOV-1994
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: KONSKI, ANTOINETTE F.
 / REGISTRATION NUMBER: 34,202
 / REFERENCE/DOCKET NUMBER: 20344-20975.00
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 813-5600
 / TELEFAX: (415) 494-0792
 / TELEX: 706141
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1711 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / US-08-342-930-2

Query Match 13.6%; Score 954; DB 2; Length 1711;
 Best Local Similarity 25.4%; Pred. No. 9,2e-53;

Matches 366; Conservative 222; Mismatches 542; Indels 315; Gaps 64;

QY 3 PAAREALPPRSPLRWALPLLLLLRLQIILCAGTSPSPIDP---SVATVATGNGT 59

Db 142 PARLEASMSD-APGDQDSYQLLLYHLSQTLAC--NVSVSPDTLSTYFGDILLPGTYVL 197
 QY QISSTAESFHKQ-----GTGTPQVETNTSEDES-----SCA 92
 Db 198 EVITWAGSLHAKTSLIOWTEBPVPPDHLALRALGSSSLQAFMNSSEGNATSHIMLTDLGG 257
 QY 93 NDSLRTEPG-----SNGTDGASQKTPSSSGPSPVDIKAVSIS---PNNVILTW 139
 Db 258 TMTTAVIRQGVSTHTFLHLSPGTP-HELKVCASAGPQIQNGPSATWETYPSPSDLTLP 316
 QY 140 KSNDTAASEYKVVYKHKNEKETTIVVHOPMCNITGLRPATSYFSIT-PGIGNETWGD 198
 Db 317 LRLNELMS-----W-KAGGADGVYKLKSGMESTITLGP 352
 QY 199 RVIVYITEPIPVSDRLVALGVKRAKLSWSNGTASCRVLLESIGSHEELTQDSRLQVN 258
 Db 353 ECNAVPPGPPLPPGHVYTLQKVLGAPYAWEGS---TWLARSALPREV----- 398
 QY 259 ISDLKPGVQVYNINPYLLQSNKTKGDDPLGTREGGLDASNTERRA--GSPTAPVHDESLVCP 316
 Db 399 ----PQARLMLD-----GLEASKQPERKRLVSDAP---GSLGN 431
 QY 317 VDPSSGOQSRDTEYLVLGLEPGRYNATVYQDANGTEGQPOAIEPRTNAIQVDYAVN 376
 Db 432 ISVPSGA---THVIFCGLVPGAHYVDI---ASSTGDISQISIGTSPPLPPQSLEVIS 483
 QY 377 ISATS-LTLWKVSDNESSNNTYKI--HYAG-----TDSNINSEPPAVIP 422
 Db 484 RSPSPDLTIAMGAPQGLEG---YKVTWHDGQSRPGDLVDLGPDLTSLTL---KSLVP 537
 QY 423 GLRSSTFYNTVCPVLGDIETGPGFLOVHTPPVPVSDFRVTYV-STTEIGLA---SSH 477
 Db 538 G-----SCYTSAMAMAGNLSDSQKHSCTRPPNLSIGFPHQALAKASHYHPPGR 593
 QY 478 DASFOQH-----TQEGAGNSRVEITNQSIILIGLFPGRYKC-FEIVPKGP 524
 Db 594 DAHLRLRLRPLTLESEKVLPREAQNFSMAQLTAG-----CEFOVLSTL 639
 QY 525 NGTE-GASRTVCGRVPSAVFDIHVVYVTTTMMWLMKS--PGASRYVYHVLIES-KHS 581
 Db 640 WGSERSSANATWTPPSAPTLVNTSDAPTOQSWAHVPGGRSRYQVTLVOESTRTAT 699
 QY 582 NHTSTYDKAITLQGLIPGLYNITISPEVDHWGDPNSTAQYTRPSNVN----- 631
 Db 700 SIMPKEDGTSFLGLPTGKYKEVIS---WAGP---LVTAAANVAMWYPLIPNEL 750
 QY 632 -IIVSTNTAATLISQNFDDASPT-XSYC-LIIEKAGNSNATQVYTDIGTDAVTEIL 688
 Db 751 LVSMQAGSAVNLMW---PSGELGQACHAQLSDGHLS--WEQPLKLGQELFMRDLT 804
 QY 689 PGSSYVEIIFAQVGD-----GIKSLPEGRKSFCTDPASMASFOCEVVPKEPALVLMKT 741
 Db 805 PGGTISMVRCRAGPLQASTHLVLSVERG-----PVE---DYLCHPEATYLLALNWT 853
 QY 742 CP-----PGANAGFELEVSSGAMNATHLESCESSNGTEYRTVYILNFS 786
 Db 854 MPAGDVVCLVYVERLVPGGTHFVQVNTS--GDALLPLNLMPT--ISYRLSTVLGRN 909
 QY 787 TSYNISITTVSGKMAAPTRNTCTGIDPPRPD--GSNITSVSHNSYKVFSGFESH 844
 Db 910 SKMSRAVSLV-----CSTSAEMHPPELAEPPOVELGTGMGVYWRGMFGKOD 957
 QY 845 GPIKAYAVILITG-BAGHPSADVLKYT-YDPEKKGASPTYVYVYLRT---BEKGRSQSL 898
 Db 958 GQIQWYGIATINMTLAPSRRAINYTDHYRRC-ESFLALFPNPFYEPNAGPRS- 1015
 QY 899 SEVLKTEIDVNE--STILGYNGKLEPLGSRACVAGFTNITHPQKGLIDGAEYSVS 956
 Db 1016 ----WTVPVGTEDDNTQELCNGRLKSGFYRFSVAFSR-----LNPETITLA 1060
 QY 957 PSRYSD---AVSLPDDP-GVIGCAVFGCIFGALVIVYVYGGTIFWR---KKRKDAKNE 1007
 Db 1061 PSFSEPRASISLAIPLTVMIGAVGSI---VIVCAVLCILRWCCKGPRSEKDGFSKE 1117

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QY 1008 VSFQIKP-----KSKLIRVENFEAYFKKQADSNCGPAEYEDLKLVGISQPKYAAELA 1063
Db 1118 -----LPPYLMWRHRPIPIHSFQSYEAKSAHAHQTFQFEELEKVGKQDPLAEHR 1172
QY 1064 ENRGKKNYNNVLPYDISRVKLSV---QTHSTDYINANNYMGYSKKDPIATQGPLPNTL 1120
Db 1173 DNIKKNYPHLPYDPHSRVRLTQLPGBPHS--DYINNFIQSYHTQDEIIATQGPLKKTLL 1230
QY 1121 KDFRMYWKKVYAIIMLTCKVEGQRTKCEYRPSKQAO-DYGGITYAAMSEIYLPEKTI 1179
Db 1231 EDFRLTWEEQOVHAIIMLTQWEMENGRVLCBHYMPANSTPYVGHITTHLLAEPEDEWTR 1230
QY 1180 RDPFKVNIQTSSEHPLRQFHTSMQDGVDPDTLLINFRYLVADYKMSPPSPILVHC 1239
Db 1291 REFQLGHTQEKQKRRVQLOLFTTPDHSVPAPSSLLAFVELVQSOVQATQCKGPILVHC 1350
QY 1240 SAGVGRGTGTAIDRLIYQIENENTVDYGVYDLRMHRPLMVQTEDOYVELNOCVLD-I 1238
Db 1351 SAGVGRGTGTAIDRLIYQIENENTVDYGVYDLRMHRPLMVQTEDOYVELNOCVLD-I 1410
QY 1299 VRSQKDS 1305
Db 1411 LKGPPDS 1417

RESULT 7
US-09-822-871-4
; Sequence 4, Application US/09822871
; Patent No. 6723547
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; FILE REFERENCE: CLO01219
; CURRENT APPLICATION NUMBER: US/09/822.871
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2301
; TYPE: PRT
; ORGANISM: Rat
US-09-822-871-4

Query Match 12.3%; Score 864; DB 4; Length 2301;
Best Local Similarity 23.5%; Pred. No. 9,6e-47;
Matches 405; Conservative 216; Mismatches 533; Indels 568; Gaps 77;

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QY 387 -----KVDNESS----- 395
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QY 396 -----NYTK-----IHVAGTDS-----NLNVEPR 418
Db 1040 KSDI IHVYTDQDIPBGPVGNLTFESISSTAIHVSWEPPSQPNGLVFYYSILNQQSPPR 1099
QY 419 AVIP-----GLRSTFNITVCPVLGIBETPG-----LOVH-----T 452
Db 1100 HMPPLVTENSIDFDDLEKTYDIFKITP-----STEGKSEYTYTQLHKTEDVPT 1154
QY 453 PPVPSDFRVTVSTTEIGLAMS-----SHDAESFQMHTIEGAGNSRVEITNQSIIIGCL 509
Db 1155 PPI-INTFK--NLSSTILSMDEPLKPNCAILGHTLTLQCPHANNHFVSGNHIVLEEL 1211
QY 510 PPGTKCFEIVPKKPNCTEGASRTVCNRYPSAVF-----DIHVVYVTTMMDWK--SP- 563
Db 1212 SPFLYSPFAARFMKGL--GPSILFPYTDSEADLPAPQNLTLINTYSDFWLWMSPSPL 1270
QY 564 DGASEYVYHLVIESKGSNHTSTYDCAIT-----LQGLIPGLNYNTTIPEDVHWGD 616
Db 1271 PGGIVKYSFKI-----HEHETDVFEYKNIISGLQTDAKLEGEPVSTSVSVAFTKVGNGN 1327
QY 617 PMS-----TAQYRPSNVSNID--VSTWTTAATLSMOPDASPTYSYCL--LIEKAGNS 668
Db 1328 QYSNVVEFTTQESVPEAVRNIECVARDQOSVVM---DPRKTNGLIIHMITVGNLS- 1383
QY 669 NATOVVTDIGITDA--TVTELIPGSYTYVEIFAQVGDGKISLEBGRKSFTCTDPASMSFD 726
Db 1384 -----TKVSPRDPTYFTTKLPNTSYVEFEVRASTAG-----EGNESRC-DISTLP--- 1428
QY 727 CEVYFKKPAVY-----LKWTCP----- 743
Db 1429 -ETVPSAPTVNAFNSVOSTSATLTWTKRDTLFGYFQNYKITTLQRAOKREMEPECEIEH 1487
QY 744 -----PG----- 745
Db 1488 QKQOYLVEANOTETVHGKLFKFRMYRFOVAASTNVGYSNASEWISTQTLPPPPGPPENV 1547
QY 746 ---ANAGELEVSQANN-----NATHLSGSSNGTEYKTE 779
Db 1548 HVATSPFGINIS---WSBPAVINGPTFYLLDVKSVDDDDDNISFLKS--NENKTI---TE 1600
QY 780 VTYLNSTSYNIST-----TVSGKKAAPFRANCTGTTGTPPP----- 818
Db 1601 INNLEVFTRYSVVITAFVGNVSRAYTDGKSABEVIITLLESVPKDPNNMTFOKIPBEVT 1660
QY 819 -----PDGSPN-----ITSVSHNSYVKFSGFEASHG- 845
Db 1661 KFOULTPEPSQPNINIRYQALVYREDDPTAVQIHNFSIIIOKTOTSIAMLEGLKGHTY 1720
QY 846 PIKAYAVLLTGEAGHSADVLKTYD-----DPKGAADTYVTVYLR-- 888
Db 1721 NISVYAI-----NSAGAPKVQMRITMDIKAPARKSKPIPIRDATGKLVSTTTIMP 1776
QY 889 -----TEEKGRSQSLSEVLKYEIDVGNES-----TTLGYN-----GKL 922
Db 1777 ICYVNDHGPTRNVQVLAETGAQOD--GNVTKWDAVFNKARPYFTMGFPNPPICEBKT 1835
QY 923 EPLGSYACVAGFNITFHPQNK-----GLIDGASVY-----SFSRYSDAV- 964
Db 1836 KFSGNBEIYVIGADNACMIPENBEKICNGPLKPKQYLFKFRATNMWQGFDSYSDYIK 1895
QY 965 -----SLPDPGVICGAVGCIFGALVYV--VGGEIFMRKKRK-----DAKNEVSF- 1010
Db 1896 TLGGLSERTVEIILSVTLICLISLILGTALFAVRIRQXKBEGTYSPPRABEIIDTFKX 1955
QY 1011 -----SQIKPKSKLIRV-----ENFEAYFKKQADSNCGPAEYEDLKLV 1051
Db 1956 LDOLITVADDELKDERLRLLSYRKSIKPISKSKSFLOHVELCTNSMLKFOBEPSSEL--- 2012

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[illegible]

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1      RESULT 8
2      US-08-201-697-4
3      ; Sequence 4, Application US/08201697
4      ; Patent No. 5705623
5      ;
6      ; GENERAL INFORMATION:
7      ; APPLICANT: Wiggins, Roger C.
8      ; APPLICANT: Thomas, Peedikayil E.
9      ; TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
10     ; TITLE OF INVENTION: 1
11     ; NUMBER OF SEQUENCES: 17
12     ;
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: Campbell and Flores
15     ; STREET: 4370 La Jolla Village Drive, Suite 700
16     ; CITY: San Diego
17     ; STATE: California
18     ; COUNTRY: USA
19     ; ZIP: 92122
20     ;
21     ; COMPUTER READABLE FORM:
22     ; MEDIUM TYPE: Floppy disk
23     ; COMPUTER: IBM PC compatible
24     ; OPERATING SYSTEM: PC-DOS/MS-DOS
25     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
26     ; CURRENT APPLICATION DATA:
27     ; APPLICATION NUMBER: US/08/201,697
28     ; FILING DATE: 25-FEB-1994
29     ; CLASSIFICATION: 530
30     ; ATTORNEY/AGENT INFORMATION:
31     ; NAME: Campbell, Cathryn A.
32     ; REGISTRATION NUMBER: 31,815
33     ; REFERENCE/DOCKET NUMBER: P-UM 9783
34     ; TELECOMMUNICATION INFORMATION:
35     ; TELEPHONE: (619) 535-9001
36     ; TELEFAX: (619) 535-8949
37     ; INFORMATION FOR SEQ ID NO: 4:
38     ; SEQUENCE CHARACTERISTICS:
39     ; LENGTH: 1188 amino acids
40     ; TYPE: amino acid
41     ; TOPOLOGY: linear
42     ;
43     ; MOLECULE TYPE: protein
44     ;
45     ; US-08-201-697-4

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	Query March	12.2%	Score 855;	DB 1;	Length 1188;	
	Best Local Similarity	28.0%	Pred. No. 1.3e-46;			
	Matches 279;	Conservative 159;	Mismatches 345;	Indels 214;	Gaps 42;	
QY	452 TPVPVVS-----DFRVTVSTTEIGLAWSHDA--ESFQHITQEGAGNSRVETT	499				
	: : : : : : : : : : : :					
Dd	271 TPEIPSGNISGMDPENSDDYETTSQPYWMOASAPASEDEFFVSLMEYEKNSTLSET	330				
	:					
QY	500 TNOSIIIGLEPGPKYCPEIIVPKNGTNEGASRTQCNTVPSAVVDIHV-----	548				
	: : : : : : : : : : :					
Dd	331 EKSISSGSFSFPVOMILTWLPKPPTADG-----FHIIIEEREKFTLEYLM	376				
	: : : : : : : : : : :					

Qy	549	VYVTTTMMIMDMXSPCAGAEYVYHVIIEKSHSNHSTYDKMTLOGLPGLTYNTTSP	608
Db	377	VDEBAHEFAELKEP---KTKLSTYTTBSSSGCETRKSQSAKSL-----SPYISB	424
Qy	609	EVDHWGDENSTAOQYTRPSNVSNIDVSTTTATLSM---ONFDDASPTYSCLLIEFA	664
Db	425	SGE---WIEILT---EKPOHVS-VHLSST-ALMSWTSQSNVNSTIYSV-VSLTCCQHQ	475
Qy	665	GUNSN-ATQVYMDIGITDITVELLPGSSYTYEIPAQVBDGKLSLEPGKSCSTDPAWA	723
Db	476	KSSQRLKEQYCTQOVNSSKPIIENLVGAQYQVYILRKPEL-----GPPS---DPVTEA	527
Qy	724	SF-----DCEVVPKEP-ALVLMKTCR-PEANAGFELEVSSGAMNNATHIESCSSENGTEY	776
Db	528	IYPTGIKDMLKPLPGTAVVLSMTPEYLGVEFKYVEME--YFNAT---MTSEYTYT	581
Qy	777	RREVTYLANFST-----VNISTVSCGMAAPRTNTCTTG---ITDPPPDG	821
Db	582	EIAAT-VSLTASVRIANLLPAMYPRFVMTWMD---PELSCDSTISFTIAY----	633
Qy	822	SPNTSVSNSTKYVFS-----GPEASHGP-KAYAVI-----LTGGEAGH	861
Db	634	ABEITSVEFNLLIYISWTYGDITDLSHRLHMMVVAEGKKIKKSVTRNVMATLISL	693
Qy	862	PSADVLKTYTDFEKKGAADYVYTLIRTE-----	890
Db	694	PGGDIYNLSVACTERGNTSMRLVLEKLEPAPKSLFAVNKTQTSVTLTWEEGVADFE	753
Qy	891	----EKGSSQSLSEVLKXEIDVGNESTLGYNGLEPLGSRACVAGFTNITPHRQNG	946
Db	754	VFCQGVSSQKTK--LQEPVAVSSHVVYI---SSLPATVYNSVTSFSH-----	798
Qy	947	LIDGAEYSVFSRYSDAVSLPQDPGVLICAGVFCIFGALVIVTVYGGFIEMRK-----RK	1001
Db	799	---DBSPVPTFLAVSTWYI-EMNPRVVIVISVLAISTLLIGLLVTLILRKHLQYARE	854
Qy	1002	DAKNNEVSFSQIKP-----KSKL---IRVENTEANYFKKOQADNSCGFAEY	1045
Db	855	CGAGTFVFALEBBDGKLPYMSKNGKLKRRKLTLPVOJDDPDAYIKMAKSDYKFSIQF	914
Qy	1046	EDLKLVGISQRYAAELAENGRKRVNNVLPRYDISRYVL-SVQHSSTQDYINANMYPGX	1104
Db	915	BEKLKIGLIDIHFPADLEPLNRCCKRYNLIIPYDSRVALVSMNEBEGADYINANYIPGX	974
Qy	1105	SKOPFIATQGLPNTLKDFWRWMEKUNYALIMLTKCYEGRTICEEYMP-SKQADQYD	1163
Db	975	SPOEIIATQGLPEPTRNDPFMWGLQKSOQIIVMLTQCNEKRKRVKCDHWMPTEBPIAYGD	1034
Qy	1164	ITVMTSEIYLPKMTIDBFTVKNIQTESHNLRFHFSWSDHVP--DTTDLILNRYL	1221
Db	1035	ITVEMISREEDDDACHFRILN--YADEMODVMEFNVTAMPDGHVPTANNAESTILQFVHM	1092
Qy	1222	VRDYMKOSPPESPILVHCSAGVGRGTGFIALDRLIYOIENENTVDYVGIYDLRMRPLM	1281
Db	1093	VRQCATKS--KGPMIHCSAGVGRGTGFIALDRLIQHRIHREFPIDLIGVSEHMSYMSM	1150
Qy	1282	VQTEDEYVFLNOCYLDIVRSQKSV---DLIYONTT	1315
Db	1151	VQTEQYIFIHQCV-QLMAMKKKQOICISDVIENVS	1186

RESULT 9
 US-09-949-016-8051
 : Sequence 8051, Application US/09949016
 : Patent No. 6812319
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: VENTER, J. Craig et al.
 :
 : TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 : WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 :
 : FILE REFERENCE: CL001307
 :
 : CURRENT APPLICATION NUMBER: US/09/949,016
 :
 : CURRENT FILING DATE: 2000-04-14

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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8051
; LENGTH: 1246
; TYPE: PRN
; ORGANISM: Human
; US-09-949-016-8051

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Query Match	Similarity	12.1%	Score 854;	DB 4;	Length 1246;
Best Local	Similarity 28.0%;	Pred. No. 1,7e+46;			
Matches	279;	Conservative 158;	Mismatches 347;	Indels 212;	Gaps 41
Qy	452	TPVPVVS-----DFRVTVSVTEIGLAWSHDA-----ESPOMHTQEGAGNSRVEIT	499		
Db	329	TPPEISGNISSGMPEDFNSSDYEETTSQPYWMPDSASAPESEDBFVSLPMEYENNSTLSET	388		
Qy	500	TNOSIIIGLPGRTKCYCEIYPKPGNGEGASRTVCNNTVSAVDIHV-----	548		
Db	389	EKSTSGSFPPVQWILTWLPPKPTAPDG-----PHIERENFTEYLM	434		
Qy	549	VYVTTTMMMLDMKSPDGASEYVYHLVLSKSGSNHTSYDKAITLQGLIPTLYNITIS	608		
Db	435	VDEAHFVVALKEP-----GKKYLSVTTSSSGSCSTRSGSKSL-----SFYISP	482		
Qy	609	EVDHWGDPNSTAQTTPRSANVSNIDVSTNTTALISM-----QNPDSAPTSYCLLEKA	664		
Db	483	SGE--WIEELT-----EKQPHVS--VHVLASLT--ALMSWTSQBNNTSTIVS-VSLTRCKQ	533		
Qy	665	GNSGN-ATQVATDIDGATVATELIPGSSYVYEIAQVGDGKSLPEPKSFCTDPASMA	723		
Db	534	KESQBLEQYCTQVNSSKPIIENLVFGAQOVVYLRGPLI-----GPPS--DPVTFPA	585		
Qy	724	SF-----DCEVVPKEP-ALVILKWTCP--PGANAGFELEVSSGAMNATHLESCSSNGTEY	776		
Db	586	IVPTGIKIDLMYPLGPPTAVVLTSMTPRYGVPRKYVEMF--YFNPAT---MTSEWTTY	639		
Qy	777	RTEVTVLNFST-----VNISTTVSCGMALPTNTCTTG---ITDPPRPDG	821		
Db	640	EIAAT-VSLTASVARIANLLPAMYINFRYMTWTWGD--PEUSCCDSSTISFTIATV---	691		
Qy	822	SPNTTSVSHNSVKYKFS-----GFEAGHCEPIKAAYI-----LTGEGAGH	861		
Db	692	APELTSVEYFNLSLIYSWTYGGDDTDLDSHSMMLHMVVAEGKKIKKSVTNVMTALISL	751		
Qy	862	PSADVLTYYDDPFKKGASDYVTVYILRPE-----	890		
Db	752	PPGDIYMLSVTACTERGSGNTSMRLVYLKEAPPKSLPFAVNKTQTSVTLTWBEGVADEFE	811		
Qy	891	-----EKGSQSLSLEVLKYEIDVGNESTLGYNGCLPELGSYRACVAGFTVTFHPQKG	946		
Db	812	VFCQVQVSSQCKT--LQEPVAVSSHYVIT-----SSLPATAYNCVTSFSH-----	856		
Qy	947	LIDGAEYSVFSRYSDAVSLPQDPGVCIGAVFGCIGALVTVYVGGFIEMWRK-----RK	1001		
Db	857	---DSPSPVPTFIAVSTWTV--EMNPRVAVVISVLAISTLLIGLLVTLILLRKHLQMAR	912		
Qy	1002	DAKNNEVSFSGIKP-----KKSXL-----IRVENFEAYRKQQAQNSGCFABEY	1044		
Db	913	CGAGTFVNFASLERDQKLPYMSKNGLKRRKLTNPVQDDPDPAYIKDMAKOSDYFSLQF	972		
Qy	1046	EDLKLVGISQCKYAAELAENRGKRRYNNVLPYDISRVKL--SVQTHSTDDYINANTMPGY	1104		
Db	973	ELKTLIGDIDIPHADLPINRCKRKYTNILPYDFSRYVLSMNEBEGADYINANYIPGIN	1033		
Qy	1105	SKQDPIATQSGELPNTLKDPFMRWMEKNAVYAILMLTKCYEQGRTKCEEYWP--SKAQDDYD	1166		
Db	1033	SPQEIATQGGPLPETERNDPFMRKVVVLAQKSKQIILVMTLQCKEKKRVCKDHWHPTEBPIA	1092		

OY	TTVAATSELVEMPTIRDPVTYNQITSESHPRKOPFTSMPDGV--DTTDLINFRYL	1221
OY	1164	
Dd	ITVETISSEODDMACRRPRT--YADEQDVMHFFNTAMPDHGFTPAANAESILOFVHM	1150
Dd	1093	
OY	VRDYKOSPPESPILVHCASAGVGRTGTFAIDRLIYQIENENTVDVGYIDYLRMRPLM	1281
OY	1222	
Dd	VRQAQTKS--KEPMIIHCASAGVGRTGTFAIDRLIYQIHIDEHPVDILGLVSEKRSTRMSM	1208
Dd	1151	
OY	VQTEBDQVFNLQC--LDIVRSQKSKVDLLIQNTT	1315
OY	1282	
Dd	VQTEBQYTFIHQCVDLMMKKKQDCISIVYEENS	1244
Dd	1209	

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US-09 RESULT 10
US-09-949-016-8052
; Sequence 8052, Application US/09949016
; Patent No. 6812359
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8052
; LENGTH: 1246
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8052
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Query Match 12.1%; Score 854; DB 4; Length 1246;
Best Local Similarity 28.0%; Pred. No. 1.7e-46;
Matches 279; Conservative 158; Mismatches 347; Indels 212; Gaps 41;

QY 452 TEPVEVS-----DFRYVAVSTTEIGLAWSSHDA-----ESFQMIITOGAGNSRVEIT 499
DB 329 TPEISGNINSSGMPDPSNDYETTSQPYWMDSAAPESEDEFVSILPEYENNSTLSET 388
QY 500 TNQSIIGGLPFGTYCFEIVPKGNGRTGASRTVCNRIVPAVFDIV-----548
DB 389 EKSTGSGSFPPVQMLTLPKPKPTAFPG-----FRIHIEREENPTEYLM 434
QY 549 YVVTITTEMMLDKSPDGDASEVYYHLYIBESKHSNHTSYDKAITLQGLPGLYNTITSP 608
DB 435 VDEAHAEVVAELKEP---GKYLSTYTTSSSGSCETRKQSASL-----SPTISP 482
QY 609 EVDHWGDPNSIAQYTRPSNVSNIDVSTNTATLTSW-----QNFDDASPTYSYCLLIEKA 664
DB 483 SGE--WIEELT---EKPGHVS--VHVLSEST--ALMSWTSQEXNYNSTIVSV--VSLTRCKQ 533
QY 665 GNSNS-ATQVATDIGITDATTTELLIPGSSYYTBEIFAQVGDGKSLBPGKRSFCTDPAUMA 723
DB 534 KESQRLKQCYCTQVNSSKRIIENLVGAGQYOVVIYLRKPLI-----GPPS---DPVTFA 585
QY 724 SF-----DCEVVPKPEP-ALVLCMTCP--PGANNGFELEVSAGANNATTHLSCSSENTEY 776
DB 586 IVPGICXDLMLYPLCPPLAVLS*WTPPYLGVFRKIVVEMP--YFNPAIT---MTSEWTTY 639
QY 777 RTEVLYLNFST-----YNISITTVSGKRAAPFTRNCTTG---ITDPPEPDG 821
DB 640 ELAAT-VSLTASVRIANLLPAMYNPFRVMTVMGMD---PELSCDSDSTISFIRAPV---- 691
QY 822 SPNTITSVHNSYKAKFS-----GEBAGGPIKAAVIT-----LITGEAGH 861

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Db      692 ABEITSVEYFNSLLYISWTYGGDTTDLSSRLMHWVAEGKKIKKSVTRNMTA1LSL 751
Qy      862 PSADVLTYYDDPKKASDYYVYTLIRTE----- 890
Db      752 PRODIYNLSVTACTEGSNTSMRLVLEBPAPKSLFANVKTQTSYTLTLMVEGVADFE 811
Qy      891 ----EKGRSOSLSEVLKYEIDVGNESSTLGYNGKLEPLGSYACVAGFTNTTFHPONGK 946
Db      812 VFCQGVSSQKTK--LQEPVAVSSHVTL-----SLLPFAVNCSTSPSH----- 856
Qy      947 LIDGASYSYFSRYSNANVLPDOPGYICAGVFCIGALVITYVGGFTFWRKK-----RK 1001
Db      857 ---DPSVPTFFIAVSTMT--EMNPVNVISVALISTLLIGLLVTLILIRKGLQMAE 912
Qy      1002 DAKNNEVSFSQIKP-----KSKL---IRVNFPAVFKQOADSNGFAEY 1045
Db      913 CGAGTFVNFASLEBROGKLPYNNKNGKRLTNVQDDPDAYIKDAAKSDYFSLQF 972
Qy      1046 EDLKVGISQPKYAELAENRGKRNYYLPIYDISRVKL-SVQTHSTDDYINANYMPGYH 1104
Db      973 BEIKLIGLDIPHPADLPINRCNRYTNILPYDFSRVRLVSNMEEGADYINANYIPGN 1032
Qy      1105 SKDPIATOGPLPNTLKDFRWVMEKNVYAILMLTKVCEQGRTKEEYTP--SKOADYGD 1163
Db      1033 SPOEYIATOGPLPBTBRNDPFWKVLQOKSQIIVMLTQCNEKRRVKCDHYMPFTEEPYAGD 1092
Qy      1164 ITVANTSEIYLPFWTIRDTFVNKIQTSSEHPLQPFHTSMPDHGP--DTTDLINFRYL 1221
Db      1093 ITVEMISEBQDDMACRHRLN--YADEMODVMHNTYAMPDGHGPTNAAESILQFVHM 1150
Qy      1222 VDDYKOSPPEPPIVHCSAGVGRGTGTFALDRLIYQIENENTVDYGIYVDLNRHPLM 1281
Db      1151 VFOQATKS--KGPMTIHCSAGVGRGTGTFALDRLLOHIRDHEFVDILGLVSEMSYSRWSM 1208
Qy      1282 VQTEQYVFLNQCY--LDIVRSQKSKVDLIYQNTT 1315
Db      1209 VQTEQYIFIHQCVOQMMKKKQCFISDIYENVS 1244

RESULT 11
US-09-949-016-8053
; Sequence 8053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8053
; LENGTH: 1246
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-8053

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Query Match 12.1%; Score 854; DB 4; Length 1246;
 Best Local Similarity 28.0%; Pred. No. 1.7e-46;
 Matches 279; Conservative 158; Mismatches 347; Indels 212; Gaps 41;

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Qy      452 TTPPVVS-----DFRYVSTTEIGLAWSSHA-----ESFQMTITOGAGNSRVEIT 499
Db      329 TPEIPSGNISGWDENFSDYETTSOPYWDMSASABESBDEFVSILPMEYENNSTLSET 388
Qy      500 TNGSIIGGLPPTGTYCFEIVPKGPNGTGASRTVCNRTVSAVFDLHV----- 548

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Db      389 EKSTSGSFFFPVQMIWLMLPFPKPTAFDG-----FHHIERENFTYIM 434
Qy      549 VYTTTMMILDMKSPDGASEYVHLVIESKGSNHTSYDAKITLQGLIPGTLNNTISP 608
Db      435 VDEBAHEFVALKEP---GKYLSVTTFSSSGSCETKRSQAKSL-----SFYISP 482
Qy      609 EVDHVMGDPNSTAQTSPSNVSNIDVSTNTTAATLSM-----QNRDDASPTYSYLLLEKA 664
Db      483 SGE--WIEBELT---EXPQHSV--VHVLSTT--ALMSWTSOENNSTIVSV--VSLTCQK 533
Qy      665 GNSSN-AQVNTDIGITADATVTELLIPGSYTVEIFAQVGDGKISLEBGRSFCDDPASA 723
Db      534 KESQRLKQCYCTQYNSKPIIENLVPGAQVQVYILAKGLI-----GPPS---DPTFA 565
Qy      724 SF-----DCEVPEP--ALVLTCTP--PGANAGELEVSAGANNATHLESSENCTEY 776
Db      586 IVPGIDMLLYPLGPFAVILSWTRPYLGVRKVVEMF--YFNPAT---MTSEWTTY 639
Qy      777 RTEVLYNFS-----YNISITVSGKMAAPTRNTCTG---ITDPPPDG 821
Db      640 EIAAT-VSLTASVRIANLPAWYTNFRVYTWNGD--PELSCDSSTISFITAIV--- 691
Qy      822 SPNTSVSHNSVKKFS-----GFEASHGPIKAYAVI-----LTGSEAGH 861
Db      692 ABEITSVEYFNSLLYISWTYGGDTTDLSSRLMHWVAEGKKIKKSVTRNMTA1LSL 751
Qy      862 PSADVLTYYDDPKKASDYYVYTLIRTE----- 890
Db      752 PPGDIYNLSVTACTERSNTSMRLVLEBPAPKSLFANVKTQTSYTLTLMVEGVADFE 811
Qy      891 ----EKGRSOSLSEVLKYEIDVGNESSTLGYNGKLEPLGSYACVAGFTNTTFHPONGK 946
Db      812 VFCQGVSSQKTK--LQEPVAVSSHVTL-----SLLPFAVNCSTSPSH----- 856
Qy      947 LIDGASYSYFSRYSNANVLPDOPGYICAGVFCIGALVITYVGGFTFWRKK-----RK 1001
Db      857 ---DPSVPTFFIAVSTMT--EMNPVNVISVALISTLLIGLLVTLILIRKGLQMAE 912
Qy      1002 DAKNNEVSFSQIKP-----KSKL---IRVNFPAVFKQOADSNGFAEY 1045
Db      913 CGAGTFVNFASLEBROGKLPYNNKNGKRLTNVQDDPDAYIKDAAKSDYFSLQF 972
Qy      1046 EDLKVGISQPKYAELAENRGKRNYYLPIYDISRVKL-SVQTHSTDDYINANYMPGYH 1104
Db      973 BEIKLIGLDIPHPADLPINRCNRYTNILPYDFSRVRLVSNMEEGADYINANYIPGN 1032
Qy      1105 SKDPIATOGPLPNTLKDFRWVMEKNVYAILMLTKVCEQGRTKEEYTP--SKOADYGD 1163
Db      1033 SPOEYIATOGPLPBTBRNDPFWKVLQOKSQIIVMLTQCNEKRRVKCDHYMPFTEEPYAGD 1092
Qy      1164 ITVANTSEIYLPFWTIRDTFVNKIQTSSEHPLQPFHTSMPDHGP--DTTDLINFRYL 1221
Db      1093 ITVEMISEBQDDMACRHRLN--YADEMODVMHNTYAMPDGHGPTNAAESILQFVHM 1150
Qy      1222 VDDYKOSPPEPPIVHCSAGVGRGTGTFALDRLIYQIENENTVDYGIYVDLNRHPLM 1281
Db      1151 VFOQATKS--KGPMTIHCSAGVGRGTGTFALDRLLOHIRDHEFVDILGLVSEMSYSRWSM 1208
Qy      1282 VQTEQYVFLNQCY--LDIVRSQKSKVDLIYQNTT 1315
Db      1209 VQTEQYIFIHQCVOQMMKKKQCFISDIYENVS 1244

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RESULT 12
US-09-949-016-8054
; Sequence 8054, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

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Qy 895 S-----OISLEVLKYEIDVGNESSTLGYNGKLEPLSGYRACVAGFTNITEHPQ 943
Db 748 ADFEVEVCQGVSGLEKLEKLEPAVSSHVITI-----SSLIPATYNGSVTSFSH----- 797
Qy 944 NKGLIDGASVYSFSYSDAVSLPQDPGVICGAVFGCIPGALVIVTVGGFIEMKK----- 999
Db 798 -----DSPVPFPIAVSTWVT-EMNNVNVVIVTALISTLLGLLVTLIIIRKKHLOM 850
Qy 1000 -RKDAKNEVSFSQIKP-----KSKL-----IRVENFEAYFKQQAODNSNGFA 1042
Db 851 ARFCAGCTFVNFASLEBDGKLPYMWKNGKRLTNPVQDLDPAIYKMAKSDYKFS 910
Qy 1043 BEYEDLTVGISOPKYAAELAEKNGKRNYNVLPYDISRYK-LSVQTHSTDDYINANYMP 1101
Db 911 LQPEBELKIGLDIPHPADLPLNRCNRYNTILPYDSRVRLISMNEBEGADYINANYIP 970
Qy 1102 GHNSKDFIATQGPPLNTLQDFMRWMEKKNVYAILMLTKVEGGRYCEBYMP-SKQAD 1160
Db 971 GYNSPOEYIATQGPPLPRTNDPFWKQVLOQKQOMIVMLTQCKEKRRVCDHWPFTEBPFA 1030
Qy 1161 YGDIYAMTSEIYLPETITDFTYKNIQTGESHPLRQFHTSWPDHGP--DTDLINL 1218
Db 1031 YGDIYEMISBEEODMAHHRFIN--YADEMODVHFNTYAMPDGHVPTANAASLLOF 1088
Qy 1219 RYLVRDYMKSOPESPILVHCSAGVGRGTGFIADRLIYOIENTVDVYGYVDLMMR 1278
Db 1089 VHVVRQATKS--KGPWIIHCSAGVGRGTGFIADRLLOHRIHBPFDILGLVSEKMSYR 1146
Qy 1279 PLMVQTEDQYVFLNQC--LDIVRSQKDSKVDLIYQNTT 1315
Db 1147 MSWQTEQYIYFIHQCVQOLMMKKKQOFCISDIYEVNVS 1185

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RESULT 15
US-09-949-016-8828
; Sequence 8828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8828
; LENGTH: 1274
; TYPE: PRN
; ORGANISM: Human
US-09-949-016-8828

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Query Match 12.0%; Score 841; DB 4; Length 1274;
Best Local Similarity 27.2%; Pred. No. 1.2e-45;
Matches 279; Conservative 159; Mismatches 346; Indels 240; Gaps 43;

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Qy 452 TPVPVPS-----DFRYVTVSTTEIGLANSSHAA-----ESFQMHITQEGAGSRVEIT 499
Db 329 TPRIPSGNISGMPDFNSDYETTSQPYWMDSAGABESBDEFVSIVPEMEYNNSTLSET 388
Qy 500 TNGSIIIGLFPGRKCFEIVPKGPNTEGASRTVCNRTVSAVEDIIV----- 548
Db 389 EKSTSGSFSFPVOMILTWLPKPKPTAFD-----FHIHREENFTEXLM 434
Qy 549 VYVTTTBMULDWKSPPDGAASEVYVHLVIESKRSNHTSTYDKATLQGLIPGLVNTITSP 608
Db 435 VDEBAHFVALKEP---GKTKLSVTTFFSSGSCETKRSQSAKSL-----SFYISF 482

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Qy 609 EVDHMGDPNSTAQYTRPSNVSNIDVSTNTTAATLSW-----QNFDDASPTYSCLILEKA 664
Db 483 SGE--WIEBELT-----EKDQHS--VHVLSTT-ALMSTSSQENANTSVI-VSLTQKQ 533
Qy 665 GNSSN-ATQVNTDIGITDAVTEILIPGSSYTVIEPAQVGDGKLSLEPKRSFCTDPASMA 723
Db 534 KESQRLKQYCTQYNSKPIIENILVPGAQYQVVIYLRKGPLI-----GPPS---DPVYFA 585
Qy 724 SF-----DCEVVPREP-ALVAKMTCR--PGANAGELEVSAGMNNATHLBSCESENGEY 776
Db 586 IVPGLKIDMLYPLGPFAVAVLSWTRPYLGVFRKTVEMP--YFNPAI---MTSEMTYY 639
Qy 777 RTEVLYLNFSTS-----YNISITVYSCSKMAAPRTNCTTG-----ITDPPPDG 821
Db 640 EIAAT-VSLTASVARIANLPAKTYNFRVYTWTD---PELSCDSSSTISITPAV----- 691
Qy 822 SPNITSVSHNSVYKFS-----GFASHGPITKAYAVI-----LTGEGAGH 861
Db 692 APEITSVYEFNSLLIYSMTYGDPTTDLSHSRMLHMVVAEGKKIKKSVTRNVTALISTL 751
Qy 862 PSADVLRKYTDDEPKKASDPTVYTYLIRTE----- 890
Db 752 PPGDIYMLSVTACTERSGNTSMRLVRLBAPPKSLPAVNKTQTSVTLWVEBEGVADFFE 811
Qy 891 -----EKGRSOSLSBEVLKYEIDVGNESSTLGYNGKLEPLSGYRACVAGFTNITEHPQNG 946
Db 812 VFQCVSSQKTK--LOEPVAVSSHVITI-----SSLIPATYNGSVTSFSH----- 856
Qy 947 LIDGASVYSFSYSDAVSLPQDPGVICGAVFG--CIFGALVIVTV----- 990
Db 857 ---DSPVPFPIAVSTWVT-EMNNVNVVIVTALISTLLGLLVTLIIIRKKHLOMARE 912
Qy 991 ---GGFIEMKKKRDAR-----NNEVSFSQIKP-----KSKL 1020
Db 913 CGAGTFVNFASLEBDGKLPYMWKRSIPAFLLPLPSCLMTDYLLAFYINPMSKNGKRL 972
Qy 1021 ---IRVENFEAYFKQQAODNSNGFAEYEDLTVGISOPKYAAELAEKNGKRNYNVLPY 1077
Db 973 TNPVQDLDPAIYKMAKSDYKFSLOPEBELKIGLDIPHPADLPLNRCNRYNTILPY 1032
Qy 1078 DISRVKL-SVQTHSTDDYINANYMPGYHKKDFIATQGPPLNTLQDFMRWMEKKNVYAI 1136
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Qy 1137 MLTKVEGGRYCEBYMP-SKQADYGDITYAMTSEIYLPETITDFTYKNIQTGESHPL 1195
Db 1093 MLTQCKEKRRVCDHWPFTEBPFAVYGDITVEMISBEEODMACRHRFIN--YADEMODV 1150
Qy 1196 ROFHTSMPDHGP--DTDLINLFRYLVRDYMKSOPESPILVHCSAGVGRGTGFIAD 1253
Db 1151 MHPNTYAMPDGHVPTANAASIILOFVHVVRQATKS--KGPWIIHCSAGVGRGTGFIAD 1208
Qy 1254 RLIIYOIENTVDVYGYVDLMMRPLMVQTEDQYVFLNQC--LDIVRSQKDSKVDLIY 1311
Db 1209 RLLOHIRDHEFVDILGLVSEKMSYRSMVQTEQYIYFIHQCVQOLMMKKKQOFCISDIY 1268
Qy 1312 QNTT 1315
Db 1269 ENVS 1272

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 10, 2005, 18:57:57 ; Search time 168 Seconds

(without alignments)
2654.891 Million cell updates/sec

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Perfect score: 7030
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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 33598853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7030	100.0	1337	15	US-10-366-547-42 Sequence 42, Appl1
2	7030	100.0	1337	16	US-10-723-606-2 Sequence 2, Appl1
3	6950	98.9	1337	15	US-10-366-547-44 Sequence 44, Appl1
4	6824	97.1	1337	14	US-10-380-501-2 Sequence 2, Appl1
5	4508.5	64.1	1238	15	US-10-366-547-47 Sequence 47, Appl1
6	4499.5	64.0	1216	15	US-10-366-547-49 Sequence 49, Appl1
7	1811	25.8	341	16	US-10-723-606-3 Sequence 3, Appl1
8	1242	17.7	1997	15	US-10-634-027-2 Sequence 2, Appl1
9	1241	17.7	1997	10	US-09-909-567B-54 Sequence 54, Appl1
10	1241	17.7	1997	16	US-10-408-765A-2135 Sequence 2135, Ap
11	1241	17.7	1997	16	US-10-497-692-4 Sequence 4, Appl1
12	1230	17.5	1450	16	US-10-497-692-14 Sequence 14, Appl1
13	1130	16.1	1118	14	US-10-245-539-2 Sequence 2, Appl1

14	1130	16.1	1118	14	US-10-245-539-8	Sequence 8, Appl1
15	1127	16.0	1093	14	US-10-245-539-4	Sequence 4, Appl1
16	969	13.8	1767	15	US-10-087-684-40	Sequence 40, Appl1
17	969	13.8	1767	15	US-10-218-779-40	Sequence 40, Appl1
18	954	13.6	1767	15	US-10-087-684-41	Sequence 41, Appl1
19	954	13.6	1767	15	US-10-218-779-41	Sequence 41, Appl1
20	924.5	13.2	1447	16	US-10-497-692-13	Sequence 13, Appl1
21	889.5	12.7	1447	16	US-10-497-692-13	Sequence 4, Appl1
22	879	12.5	1912	17	US-10-772-636-64	Sequence 64, Appl1
23	878.5	12.5	312	15	US-10-634-027-6	Sequence 6, Appl1
24	878.5	12.5	319	15	US-10-634-027-7	Sequence 7, Appl1
25	864	12.3	2301	10	US-09-822-871-4	Sequence 4, Appl1
26	864	12.3	2301	15	US-10-673-885-4	Sequence 4, Appl1
27	864	12.3	2302	15	US-10-087-684-37	Sequence 37, Appl1
28	864	12.3	2302	15	US-10-218-779-37	Sequence 37, Appl1
29	854	12.1	1188	15	US-10-331-496A-79	Sequence 79, Appl1
30	854	12.1	1188	16	US-10-789-241-34	Sequence 34, Appl1
31	831.5	11.8	2281	15	US-10-087-684-6	Sequence 6, Appl1
32	831.5	11.8	2281	15	US-10-218-779-6	Sequence 6, Appl1
33	827	11.8	2299	15	US-10-466-759-2	Sequence 2, Appl1
34	826	11.7	2291	10	US-09-822-871-2	Sequence 2, Appl1
35	826	11.7	2291	15	US-10-673-885-2	Sequence 2, Appl1
36	826	11.7	2300	15	US-10-087-684-10	Sequence 10, Appl1
37	826	11.7	2300	15	US-10-218-779-10	Sequence 10, Appl1
38	817	11.6	1367	15	US-10-369-493-5508	Sequence 5508, Ap
39	817	11.6	1367	15	US-10-369-493-5509	Sequence 5509, Ap
40	799	11.4	1948	9	US-09-808-602-55	Sequence 55, Appl1
41	799	11.4	1948	10	US-09-800-198-45	Sequence 45, Appl1
42	792.5	11.3	1897	17	US-10-482-029-52	Sequence 52, Appl1
43	788.5	11.2	1907	15	US-10-291-265-250	Sequence 250, App
44	782	11.1	310	9	US-09-788-626-15	Sequence 15, Appl1
45	778.5	11.1	1502	9	US-09-808-602-54	Sequence 54, Appl1

ALIGNMENTS

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RESULT 1
US-10-366-547-42
; Sequence 42, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366,547
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 1337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-547-42
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DB	1	MKPAREARLPKPSGLRMA	PLLLLRLLRQII	CAGTSPSPIDPSVATVATGNGTQ 60
QY	61	ISSTAESFKONGCTPOVETNTSEDGSSGANDSLRTPGCSNGTDCASQKTPSSTPS 120		
DB	61	ISSTAESFKONGCTPOVETNTSEDGSSGANDSLRTPGCSNGTDCASQKTPSSTPS 120		
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DB	121	PVPDIKAVSIPNTVILTWKSNDRPAASRYKTVVGHKMEKNTITVHVQPCNITGLRPAT 180		

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 DB 241 ESIGSHEELTODSRLOVNI SDLPKVQVYNINPYLQSNKTKGDP LGTEBGLDASNTERRS 300
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 DB 301 AGSPPTAVHDESLVGVDPSSGQOSRDTEVLVGLPEGTRNATVYSQANGTGEPQAI 360
 QY 361 EFRNTAIOVFDYAVNISATSLTLIMKVS DNSSSNYYTKIHVAGETDSSNINVEPRAY 420
 DB 361 EFRNTAIOVFDYAVNISATSLTLIMKVS DNSSSNYYTKIHVAGETDSSNINVEPRAY 420
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 DB 421 IGLRSTSTYNTVTCVGLDIEGTGFLQVHTPPVPVSDFRVTVSTTEIGLAWSHDAE 480
 QY 481 SFQMHITOGAGNSRVEITTNOSIIIGLFPGTXYCFEIVPGPMTGASRTVCNRTVP 540
 DB 481 SFQMHITOGAGNSRVEITTNOSIIIGLFPGTXYCFEIVPGPMTGASRTVCNRTVP 540
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 QY 601 LYNITISPEVDHVMQDPSNTAOTRPSNVSNIDVSTNTTAATLSQONDDASPTYSYCLL 660
 DB 601 LYNITISPEVDHVMQDPSNTAOTRPSNVSNIDVSTNTTAATLSQONDDASPTYSYCLL 660
 QY 661 IEKAGNSNNAQOVVTDIGITDATVTELLPGSSYVTEIFAQVGDGKSLPEPKRKSCTDPA 720
 DB 661 IEKAGNSNNAQOVVTDIGITDATVTELLPGSSYVTEIFAQVGDGKSLPEPKRKSCTDPA 720
 QY 721 SMASDCEVVPKEPALVLTWCPCPGANAGFELEVSSGAMNNATHLESCSENGETEYRTREV 780
 DB 721 SMASDCEVVPKEPALVLTWCPCPGANAGFELEVSSGAMNNATHLESCSENGETEYRTREV 780
 QY 781 TYLANSTSYNISITTVSCGKMAAPRNTCTGITDPPRPPDSPNITSYSHSVYKYSRGF 840
 DB 781 TYLANSTSYNISITTVSCGKMAAPRNTCTGITDPPRPPDSPNITSYSHSVYKYSRGF 840
 QY 841 EASHGPRIKAYAVIILTTGAGHPSADVLKTYDDPFKKGASDYYVYLLIRTEKKGQSLSLSE 900
 DB 841 EASHGPRIKAYAVIILTTGAGHPSADVLKTYDDPFKKGASDYYVYLLIRTEKKGQSLSLSE 900
 QY 901 VLKKEIDVGNSTTLGYNKGLEPLGSTRACVAGFTNITTHPQNGCLIDGASVYSPSRY 960
 DB 901 VLKKEIDVGNSTTLGYNKGLEPLGSTRACVAGFTNITTHPQNGCLIDGASVYSPSRY 960
 QY 961 SDAVSLPDGPVIGCAVFGCIFGALVITVVGFI FMRKCRDADANNEVSFQIPEKSKL 1020
 DB 961 SDAVSLPDGPVIGCAVFGCIFGALVITVVGFI FMRKCRDADANNEVSFQIPEKSKL 1020
 QY 1021 IRVENFEAYFFKQOADSNGFASEYEDLKLVGISQPYAAELANRGNRYNNVLPYDIS 1080
 DB 1021 IRVENFEAYFFKQOADSNGFASEYEDLKLVGISQPYAAELANRGNRYNNVLPYDIS 1080
 QY 1081 RVKLSVQTHSTDDYINANNVMPGYSKODFIATOGPLNNTLKDFPRMWMKNVYAIIMLTG 1140
 DB 1081 RVKLSVQTHSTDDYINANNVMPGYSKODFIATOGPLNNTLKDFPRMWMKNVYAIIMLTG 1140
 QY 1141 CVEQGRKCEBYWPSKQADYDITVAMTSEIIVPEWTIRDFYKNIQTSSEHPLROFHF 1200
 DB 1141 CVEQGRKCEBYWPSKQADYDITVAMTSEIIVPEWTIRDFYKNIQTSSEHPLROFHF 1200
 QY 1201 TSWPDHGVPTTDLINFRYLVARDYMQSPESPESPIVHCSAGVGRGTFTAIIDLRYQIE 1260
 DB 1201 TSWPDHGVPTTDLINFRYLVARDYMQSPESPESPIVHCSAGVGRGTFTAIIDLRYQIE 1260

QY 1261 NENTVDYGIYDILRMHRLPMAVOTEDQVFLNOCVLDIRSQKSKVDLIYQNTTAMTIY 1320
 DB 1261 NENTVDYGIYDILRMHRLPMAVOTEDQVFLNOCVLDIRSQKSKVDLIYQNTTAMTIY 1320
 QY 1321 ENLAPVTTFGKNGYIA 1337
 DB 1321 ENLAPVTTFGKNGYIA 1337
 RESULT 2
 US-10-723-606-2
 ; Sequence 2, Application US/10723606
 ; Publication No. US20040161821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas K.
 ; TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE
 ; TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS
 ; FILE REFERENCE: 200125 447
 ; CURRENT APPLICATION NUMBER: US/10/723,606
 ; CURRENT FILING DATE: 2003-11-26
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 1337
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-723-606-2
 Query Match 100.0%; Score 7030; DB 16; Length 1337;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKPAAERARLPSPSPGIRWALPLLLLRGLGQILCAGTSPPIPDPSVATVATGENGITQ 60
 DB 1 MKPAAERARLPSPSPGIRWALPLLLLRGLGQILCAGTSPPIPDPSVATVATGENGITQ 60
 QY 61 ISSTASFHKQNGTGPVQVETNTSEDESSGANDSLRTEQSGNGTDGASQKTPSSGTGS 120
 DB 61 ISSTASFHKQNGTGPVQVETNTSEDESSGANDSLRTEQSGNGTDGASQKTPSSGTGS 120
 QY 121 PVFDIKAVSISPNTVILLTWKSNDDTAASEYKYVVKHMEKNETITVVOHPCNITGIRPAT 180
 DB 121 PVFDIKAVSISPNTVILLTWKSNDDTAASEYKYVVKHMEKNETITVVOHPCNITGIRPAT 180
 QY 181 SYFESITPGIGNETWGPRIYKITEPIPVSDLRVALTGVRAALSWNGNGTASGRVLL 240
 DB 181 SYFESITPGIGNETWGPRIYKITEPIPVSDLRVALTGVRAALSWNGNGTASGRVLL 240
 QY 241 ESIGSHEELTODSRLOVNI SDLPKVQVYNINPYLQSNKTKGDP LGTEBGLDASNTERRS 300
 DB 241 ESIGSHEELTODSRLOVNI SDLPKVQVYNINPYLQSNKTKGDP LGTEBGLDASNTERRS 300
 QY 301 AGSPPTAVHDESLVGVDPSSGQOSRDTEVLVGLPEGTRNATVYSQANGTGEPQAI 360
 DB 301 AGSPPTAVHDESLVGVDPSSGQOSRDTEVLVGLPEGTRNATVYSQANGTGEPQAI 360
 QY 361 EFRNTAIOVFDYAVNISATSLTLIMKVS DNSSSNYYTKIHVAGETDSSNINVEPRAY 420
 DB 361 EFRNTAIOVFDYAVNISATSLTLIMKVS DNSSSNYYTKIHVAGETDSSNINVEPRAY 420
 QY 421 IGLRSTSTYNTVTCVGLDIEGTGFLQVHTPPVPVSDFRVTVSTTEIGLAWSHDAE 480
 DB 421 IGLRSTSTYNTVTCVGLDIEGTGFLQVHTPPVPVSDFRVTVSTTEIGLAWSHDAE 480
 QY 481 SFQMHITOGAGNSRVEITTNOSIIIGLFPGTXYCFEIVPGPMTGASRTVCNRTVP 540
 DB 481 SFQMHITOGAGNSRVEITTNOSIIIGLFPGTXYCFEIVPGPMTGASRTVCNRTVP 540
 QY 541 SAVFDIHVVYVTTTMMWLDKMSPDGASEVYVHLVIESKHGSHNTSTYDKALITLQGLIGT 600
 DB 541 SAVFDIHVVYVTTTMMWLDKMSPDGASEVYVHLVIESKHGSHNTSTYDKALITLQGLIGT 600

QY 601 LYNITISPEVDHVGDPNSTAQYTRPSNVSNIDVSTNTAATLSMWFDDASPTYCYCL 660
DB 601 LYNITISPEVDHVGDPNSTAQYTRPSNVSNIDVSTNTAATLSMWFDDASPTYCYCL 660
QY 661 IEKAGNSNATQVVTIDGIDATVTELI PGSSYTYVEIFAQVGDGKSLERPKSFCTDPA 720
DB 661 IEKAGNSNATQVVTIDGIDATVTELI PGSSYTYVEIFAQVGDGKSLERPKSFCTDPA 720
QY 721 SMASFDCEVVPKEPALVLTGEGHPSADVLKTYDDPKKASDTYTYVLI RTEBKGSQSISE 900
DB 721 SMASFDCEVVPKEPALVLTGEGHPSADVLKTYDDPKKASDTYTYVLI RTEBKGSQSISE 900
QY 781 TYLNFSTSYNISITTVSCGKMAAFTRNCTTGITDPPPDGSPNITSVSHSVYKVSFSGF 840
DB 781 TYLNFSTSYNISITTVSCGKMAAFTRNCTTGITDPPPDGSPNITSVSHSVYKVSFSGF 840
QY 841 EASHGPIKAAVAVILTTGEGHPSADVLKTYDDPKKASDTYTYVLI RTEBKGSQSISE 900
DB 841 EASHGPIKAAVAVILTTGEGHPSADVLKTYDDPKKASDTYTYVLI RTEBKGSQSISE 900
QY 901 VLKKEIDVGNESSTLIGYNGKLEPLGSRACVAGFTNITTHPQNGKIDGAEYSVSFSRY 960
DB 901 VLKKEIDVGNESSTLIGYNGKLEPLGSRACVAGFTNITTHPQNGKIDGAEYSVSFSRY 960
QY 961 SDAVSLPQDPGVICGAVFGCIFGALVITVVGGFIFMRKGRKDAKNNNEVSFSQIKPKSKL 1020
DB 961 SDAVSLPQDPGVICGAVFGCIFGALVITVVGGFIFMRKGRKDAKNNNEVSFSQIKPKSKL 1020
QY 1021 IRVENFEAYFPKQOADSNCGFAEEYEDKLVGISQPKYAELENNGRNRYNVL PYDIS 1080
DB 1021 IRVENFEAYFPKQOADSNCGFAEEYEDKLVGISQPKYAELENNGRNRYNVL PYDIS 1080
QY 1081 RYKLSVQTHSTDDYTNANMFGYHSKQFIATQGPRLPNTLDFMRMWEKRVVAIIMLT 1140
DB 1081 RYKLSVQTHSTDDYTNANMFGYHSKQFIATQGPRLPNTLDFMRMWEKRVVAIIMLT 1140
QY 1141 CVEGRTKCEBYWSPKQADQYDITVAMTSEI VPEWTRIDFTYVNIQTSSEHPLRQPHF 1200
DB 1141 CVEGRTKCEBYWSPKQADQYDITVAMTSEI VPEWTRIDFTYVNIQTSSEHPLRQPHF 1200
QY 1201 TSWPDHGVPTDILLINFRYLVRDYMKSPPESPILVHCSAGVRTGTFIAIDRLIYQIE 1260
DB 1201 TSWPDHGVPTDILLINFRYLVRDYMKSPPESPILVHCSAGVRTGTFIAIDRLIYQIE 1260
QY 1261 NENTVDVYGIYDLMRRLPLMVQTEDOYVFLNQCVLDIRSQKSDKVDLIYQNTTAMTIIY 1320
DB 1261 NENTVDVYGIYDLMRRLPLMVQTEDOYVFLNQCVLDIRSQKSDKVDLIYQNTTAMTIIY 1320
QY 1321 ENLAPVTTFGKTINGYIA 1337
DB 1321 ENLAPVTTFGKTINGYIA 1337

RESULT 3
US-10-366-547-44

Sequence 44, Application US/10366547
Publication No. US20030215899A1
GENERAL INFORMATION:
APPLICANT: Meng, Tzu-Ching
APPLICANT: Tonks, Nicholas K.
APPLICANT: Cool, Deborah E.
TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
FILE REFERENCE: 200125.439
CURRENT APPLICATION NUMBER: US/10/366.547
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 1337
TYPE: PRT
ORGANISM: Homo sapiens

US-10-366-547-44

Query Match 98.9%; Score 6950; DB 15; Length 1337;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1325; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKPARBARLPPRSPGRLMALPLLILLRLGQILCAGGTSPPIPDPSVATVANGENGITQ 60
DB 1 MKPARBARLPPRSPGRLMALPLLILLRLGQILCAGGTSPPIPDPSVATVANGENGITQ 60
QY 61 ISSTAESFHKONGTGTQVETNTSEDESSGANDSLTPEOGSNGTGAQKTSSTGPS 120
DB 61 ISSTAESFHKONGTGTQVETNTSEDESSGANDSLTPEOGSNGTGAQKTSSTGPS 120
QY 121 PVFDIKAVSISPTNVLITWMSNDTAASEYKVVGHKNEKXTIVVHQPNCNITGLPAT 180
DB 121 PVFDIKAVSISPTNVLITWMSNDTAASEYKVVGHKNEKXTIVVHQPNCNITGLPAT 180
QY 181 SYVESITPGIGNETWGPVYIKVITEBIPVSDLRVALTVRKALSMNNGTASCYVL 240
DB 181 SYVESITPGIGNETWGPVYIKVITEBIPVSDLRVALTVRKALSMNNGTASCYVL 240
QY 241 ESTGSHELTQDSRLQVNI SDLKRGVQYININPYLLQSNKTKGDP LGTEGGLDASNTSR 300
DB 241 ESTGSHELTQDSRLQVNI SDLKRGVQYININPYLLQSNKTKGDP LGTEGGLDASNTSR 300
QY 301 AGSPTAVHDESLVGPVDPSSGQSRDTEVVLVLEBGTYYNATVYGOAANGTEGQPOAI 360
DB 301 AGSPTAVHDESLVGPVDPSSGQSRDTEVVLVLEBGTYYNATVYGOAANGTEGQPOAI 360
QY 361 EFRTNALQVETVAVNISATSLTILMKVSDNESSNTYKIHVAGETDSSNLVSEPRV 420
DB 361 EFRTNALQVETVAVNISATSLTILMKVSDNESSNTYKIHVAGETDSSNLVSEPRV 420
QY 421 IPRGRSSTFNITVCPVLGDI EGTGPGLOVHTTPVPVSDRVTVVSTTEIGLASSHDAE 480
DB 421 IPRGRSSTFNITVCPVLGDI EGTGPGLOVHTTPVPVSDRVTVVSTTEIGLASSHDAE 480
QY 481 SFQWHTIOBAGNSRVEITTNOSIIIGLPGTGYCEIYPKGNGTEGASRTVCNRTVP 540
DB 481 SFQWHTIOBAGNSRVEITTNOSIIIGLPGTGYCEIYPKGNGTEGASRTVCNRTVP 540
QY 541 SAVEDIHVVVYTTTMMLDKMSPDGASEYVHLVIBSKHGSNHTYDKAITLQGLPGT 600
DB 541 SAVEDIHVVVYTTTMMLDKMSPDGASEYVHLVIBSKHGSNHTYDKAITLQGLPGT 600
QY 601 LYNITISPEVDHVGDPNSTAQYTRPSNVSNIDVSTNTAATLSMWFDDASPTYCYCL 660
DB 601 LYNITISPEVDHVGDPNSTAQYTRPSNVSNIDVSTNTAATLSMWFDDASPTYCYCL 660
QY 661 IEKAGNSNATQVVTIDGIDATVTELI PGSSYTYVEIFAQVGDGKSLERPKSFCTDPA 720
DB 661 IEKAGNSNATQVVTIDGIDATVTELI PGSSYTYVEIFAQVGDGKSLERPKSFCTDPA 720
QY 721 SMASFDCEVVPKEPALVLTGEGHPSADVLKTYDDPKKASDTYTYVLI RTEBKGSQSISE 900
DB 721 SMASFDCEVVPKEPALVLTGEGHPSADVLKTYDDPKKASDTYTYVLI RTEBKGSQSISE 900
QY 781 TYLNFSTSYNISITTVSCGKMAAFTRNCTTGITDPPPDGSPNITSVSHSVYKVSFSGF 840
DB 781 TYLNFSTSYNISITTVSCGKMAAFTRNCTTGITDPPPDGSPNITSVSHSVYKVSFSGF 840
QY 841 EASHGPIKAAVAVILTTGEGHPSADVLKTYDDPKKASDTYTYVLI RTEBKGSQSISE 900
DB 841 EASHGPIKAAVAVILTTGEGHPSADVLKTYDDPKKASDTYTYVLI RTEBKGSQSISE 900
QY 901 VLKKEIDVGNESSTLIGYNGKLEPLGSRACVAGFTNITTHPQNGKIDGAEYSVSFSRY 960
DB 901 VLKKEIDVGNESSTLIGYNGKLEPLGSRACVAGFTNITTHPQNGKIDGAEYSVSFSRY 960
QY 961 SDAVSLPQDPGVICGAVFGCIFGALVITVVGGFIFMRKGRKDAKNNNEVSFSQIKPKSKL 1020
DB 961 SDAVSLPQDPGVICGAVFGCIFGALVITVVGGFIFMRKGRKDAKNNNEVSFSQIKPKSKL 1020

QY 1021 IRVENEFAVKKQADNSCGFAEEYEDLKLVGISOPKAAELAENRKNRYNNVLPYDIS 1080
Db 1021 IRVENEFAVKKQADNSCGFAEEYEDLKLVGISOPKAAELAENRKNRYNNVLPYDIS 1080
QY 1081 RVLASVQSTHSDYINANVMPGHSKKDPFATQGPPLNTLKFPMRWMEKKNVYAIIMLTRK 1140
Db 1081 RVLASVQSTHSDYINANVMPGHSKKDPFATQGPPLNTLKFPMRWMEKKNVYAIIMLTRK 1140
QY 1141 CVEQGRKCEYVPSKQADYGDITVAMTSEIYLPMTIRDFVKNQIOTSESHPLROFHF 1200
Db 1141 CVEQGRKCEYVPSKQADYGDITVAMTSEIYLPMTIRDFVKNQIOTSESHPLROFHF 1200
QY 1201 TSWPDHGVDPDTDLINFRYLVADYMKOSPSPSPILVHCSAGVGRGTFTIADRLIYOIE 1260
Db 1201 TSWPDHGVDPDTDLINFRYLVADYMKOSPSPSPILVHCSAGVGRGTFTIADRLIYOIE 1260
QY 1261 NENTVAVGIVDLMHRPLMOTEDOVYELNOCVDIYRSQKDSKVDLIYONTAMTY 1320
Db 1261 NENTVAVGIVDLMHRPLMOTEDOVYELNOCVDIYRSQKDSKVDLIYONTAMTY 1320
QY 1321 ENLAPVTFGKTNGYIA 1337
Db 1321 ENLAPVTFGKTNGYIA 1337

RESULT 4

US-10-390-501-2
Sequence 2, Application US/10390501
Publication No. US20030148491A1
GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K.

TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE
PHOSPHATASES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group PLLC
STREET: Suite 6300, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 980104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/390,501
FILING DATE: 13-Mar-2003

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Roseman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058

REFERENCE/DOCKET NUMBER: 200125.402C2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: Protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-390-501-2

Query Match 97.1%; Score 6824; DB 14; Length 1337;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1302; Conservative 6; Mismatches 29; Indels 0; Gaps 0;

QY 1 MKPAREARLPSPRSGLMALPLLLLLRLGQILCAGTSPSPIDPSAVATATGSENGITQ 60

QY 1 MKPAREARLPSPRSGLMALPLLLLLRLGQILCAGTSPSPIDPSAVATATGSENGITQ 60

Db 1 MKPAREARLPSPRSGLMALPLLLLLRLGQILCAGTSPSPIDPSAVATATGSENGITQ 60
QY 61 ISSTASHKONGCTGTPVETNTSEDESSGANDSLRTEOGSNGTDGASQKTPSSGPS 120
Db 61 ISSTASHKONGCTGTPVETNTSEDESSGANDSLRTEOGSNGTDGASQKTPSSGPS 120
QY 121 PVFDKAVSISPTNVILTKSNDTRASEYKVVGHKMEKNTITVHQPCNITGLPAT 180
Db 121 PVFDKAVSISPTNVILTKSNDTRASEYKVVGHKMEKNTITVHQPCNITGLPAT 180
QY 181 SVPSITPGIGNETWGDPRVILKITEPIVSDLEVALTGVRKALSMWNGTASCRVLL 240
Db 181 SVPSITPGIGNETWGDPRVILKITEPIVSDLEVALTGVRKALSMWNGTASCRVLL 240
QY 241 ESIGSHEELTQDSLRQVNIIDLKPGVOYNINPYLLQSNKTKGDLTEGGLDASNTSR 300
Db 241 ESIGSHEELTQDSLRQVNIIDLKPGVOYNINPYLLQSNKTKGDLTEGGLDASNTSR 300
QY 301 AGSPAPVHDSLVGPVDPSSGQSRDPEVLLVGLPEGTGRYNATVYSQAANGTEGQPAI 360
Db 301 AGSPAPVHDSLVGPVDPSSGQSRDPEVLLVGLPEGTGRYNATVYSQAANGTEGQPAI 360
QY 361 EFRTNALQVFDVAVNISATSLTILMKVSDNESSNTYKIHVAGETDSSNLVSEBRAV 420
Db 361 EFRTNALQVFDVAVNISATSLTILMKVSDNESSNTYKIHVAGETDSSNLVSEBRAV 420
QY 421 IPRGSSFTFNIITCPVLGDIETGRGLOVHTPPVSDRRVYVSTTEGLAMSSHDAE 480
Db 421 IPRGSSFTFNIITCPVLGDIETGRGLOVHTPPVSDRRVYVSTTEGLAMSSHDAE 480
QY 481 SPQWHTQEGAGNSRVEITTNOSIIIGLPFGTKYCEIYKPKPNGTEGASRTVCNRTVP 540
Db 481 SPQWHTQEGAGNSRVEITTNOSIIIGLPFGTKYCEIYKPKPNGTEGASRTVCNRTVP 540
QY 541 SAVDIDHVVYTTTMMMLDMKSPDGASEYVYHVLVIESKHSNHTSTYDKAITLQGLPGT 600
Db 541 SAVDIDHVVYTTTMMMLDMKSPDGASEYVYHVLVIESKHSNHTSTYDKAITLQGLPGT 600
QY 601 LYNITISPEVDHWGDNSTAOYTRPSNVSNIVSTNTTAATLSMWNFDPDASTYSYCLL 660
Db 601 LYNITISPEVDHWGDNSTAOYTRPSNVSNIVSTNTTAATLSMWNFDPDASTYSYCLL 660
QY 661 IEKAGNSNATQVVTDTIGTDAITVTELIIPGSSYTVELFAQVGDGIXLSBGRKSFCTDPA 720
Db 661 IEKAGNSNATQVVTDTIGTDAITVTELIIPGSSYTVELFAQVGDGIXLSBGRKSFCTDPA 720
QY 721 SMASFDCEVVPKBPALVLMKTCPPGANAGRELEVSSGAMNNAHTLSCSENGTEYRTYEV 780
Db 721 SMASFDCEVVPKBPALVLMKTCPPGANAGRELEVSSGAMNNAHTLSCSENGTEYRTYEV 780
QY 781 TYINFSTSYNISITTVSCGMAAPTRNTCTGTGTPPPDGSPNITSVSHNSKYKVFSGF 840
Db 781 TYINFSTSYNISITTVSCGMAAPTRNTCTGTGTPPPDGSPNITSVSHNSKYKVFSGF 840
QY 841 EASHGPIKAYAVILTTGEAGHPADVLKTYDDPFKGAASDTYVTLIRTEBKRSGQSLSE 900
Db 841 EASHGPIKAYAVILTTGEAGHPADVLKTYDDPFKGAASDTYVTLIRTEBKRSGQSLSE 900
QY 901 VLKYEIDVGNESITLGYVNGKLEPLGSYRACVAFNITFHPONKLLIGASYSVSFSY 960
Db 901 VLKYEIDVGNESITLGYVNGKLEPLGSYRACVAFNITFHPONKLLIGASYSVSFSY 960
QY 961 SDAVSLPQDPGVLCGAVFGCIFGALVIVTVGGEIFWRKRXDKAKNNEVFSQIKPKGSKL 1020
Db 961 SDAVSLPQDPGVLCGAVFGCIFGALVIVTVGGEIFWRKRXDKAKNNEVFSQIKPKGSKL 1020
QY 1021 IRVENEFAVKKQADNSCGFAEEYEDLKLVGISOPKAAELAENRKNRYNNVLPYDIS 1080
Db 1021 IRVENEFAVKKQADNSCGFAEEYEDLKLVGISOPKAAELAENRKNRYNNVLPYDIS 1080
QY 1081 RVLASVQSTHSDYINANVMPGHSKKDPFATQGPPLNTLKFPMRWMEKKNVYAIIMLTRK 1140
Db 1081 RVLASVQSTHSDYINANVMPGHSKKDPFATQGPPLNTLKFPMRWMEKKNVYAIIMLTRK 1140

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Db      1081 RVLKSVQTHSDTDYINANNYMPGYSKQDFIATQGPLPTLKDFFRMWMEKVVAAIIMLTk 1140
Qy      1141 CVEGGRKCEBYWPSKQADYDITVAMTSEIVLPEWTIRDFYKNIQTSSHPLRQPHF 1200
Db      1141 CVEGGRKCEBYWPSKQADYDITVAMTSEIVLPEWTIRDFYKNIQTSSHPLRQPHF 1200
Qy      1201 TSWPDHGVDPDTDLINFRYLVRDYMKSPPESPILVHCSAGVGTGFFIADIRLIYQIE 1260
Db      1201 TSWPDHGVDPDTDLINFRYLVRDYMKSPPESPILVHCSAGVGTGFFIADIRLIYQIE 1260
Qy      1261 NENTADVYGIYVDLRMRHPLMVGOTEDQYVFLNQCVLDIVRSQKSKVDLIYQNTTAMTY 1320
Db      1261 NENTADVYGIYVDLRMRHPLMVGOTEDQYVFLNQCVLDIVRSQKSKVDLIYQNTTAMTY 1320
Qy      1321 ENLAPVTTFGKTNGYIA 1337
Db      1321 ENLAPVTTFGKTNGYIA 1337

RESULT 5
US-10-366-547-47
; Sequence 47, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366.547
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 1238
; TYPE: PRt
; ORGANISM: Mus musculus
US-10-366-547-47

Query Match      64.1%; Score 4508.5; DB 15; Length 1238;
Best Local Similarity 67.2%; Pred. No. 2.1e-268;
Matches 901; Conservative 108; Mismatches 226; Indels 105; Gaps 12;

Qy      1 MKPAAREKRLPPRSPGRLMALPLILLRLRQILLCAGTSPSPIDPSVAATATGENGITQ 60
Db      1 MKPAAREKRLPPRSPGRLMALPLILLRLRQILLCAGTSPSPIDPSVAATATGENGITQ 60
Qy      61 ISSTAESFHQNGTGPQVETNTSEDSGSGANDSLRTPGQSGNGTGDASQKTPSSTGPS 120
Db      61 ISSTAESFHQNGTGPQVETNTSEDSGSGANDSLRTPGQSGNGTGDASQKTPSSTGPS 120
Qy      44 ----- 43
Db      44 ----- 43
Qy      121 PVFDIKAVSISPTVILITWKSNDTAASEYKVVYKHMEKNTITTVHQPMCNITGLRPAT 180
Db      121 PVFDIKAVSISPTVILITWKSNDTAASEYKVVYKHMEKNTITTVHQPMCNITGLRPAT 180
Qy      44 --FIEAV--VSPVTLTWKHNDSGASCCR--IEKMESNLTFPVKQNTSCNITGLSPGT 98
Db      44 --FIEAV--VSPVTLTWKHNDSGASCCR--IEKMESNLTFPVKQNTSCNITGLSPGT 98
Qy      181 SYVSITIGTIGNETWGTGPRVIVKVTPEIPVSDLRALTGVRKAALSMNGNGTASCRLL 240
Db      181 SYVSITIGTIGNETWGTGPRVIVKVTPEIPVSDLRALTGVRKAALSMNGNGTASCRLL 240
Qy      99 SYTFSIISVTNETLTK-----TITTEPWPVSDLHTVSGVTOARLTWSNAGTASRYRLI 154
Db      99 SYTFSIISVTNETLTK-----TITTEPWPVSDLHTVSGVTOARLTWSNAGTASRYRLI 154
Qy      241 ESIGSHEELTQDSRLQVNIISDLKPGVQVINPYLL--QSNKTKGDPDLGTGEGGLDASNTERS 299
Db      241 ESIGSHEELTQDSRLQVNIISDLKPGVQVINPYLL--QSNKTKGDPDLGTGEGGLDASNTERS 299
Qy      155 EELTTHS-----SVNISGLKPGTN--NTFAPPESENETQADPAVAEEVPDANGTKRI 203
Db      155 EELTTHS-----SVNISGLKPGTN--NTFAPPESENETQADPAVAEEVPDANGTKRI 203
Qy      300 RAGSPFAVHDESLVGPVDPSSGQGSRDTEVLVLGLEBGTRYNATVYSQAANGTEGQPOA 359
Db      300 RAGSPFAVHDESLVGPVDPSSGQGSRDTEVLVLGLEBGTRYNATVYSQAANGTEGQPOA 359
Qy      204 PV-TVLSQLHKNSLYS--VDPSPGQDPSLTLEILLTDKPDQYNATVYSQAANGTEGQPRN 261
Db      204 PV-TVLSQLHKNSLYS--VDPSPGQDPSLTLEILLTDKPDQYNATVYSQAANGTEGQPRN 261
Qy      360 IEFPRNAIQVDFVYAVNISATSLTITKVSNDNESSANTYKIHVAGETDSSNLNVSERRA 419
Db      360 IEFPRNAIQVDFVYAVNISATSLTITKVSNDNESSANTYKIHVAGETDSSNLNVSERRA 419
Qy      262 KVFKNSTQVSDVRAVNISASSMTLTWKSNDGSHTSIVYKIHVAGGTHSVNQTNNKTEA 321
Db      262 KVFKNSTQVSDVRAVNISASSMTLTWKSNDGSHTSIVYKIHVAGGTHSVNQTNNKTEA 321
Qy      420 VIPGLRSTFYNITVCPVIGDIEGTFGLQVHTPVPVPSDFRVYVSTTEIGLAWSSHDA 479

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Db      322 IILGLSSSTLYNITVHPFLQGTGTEGPEFLQVYVSPDQVDFRVYVNSTRAIIGLAMSND 381
Qy      480 ESPQMHITQAGANSRVEITNQSIIIGLPGPKYCFEELVPGKPNTEGASRTVCARTV 539
Db      382 KSFEIFIKQDGGEGRRNASTGNOSYWEDELPKGTSHFELIIPKPGDTEGLSTVNGSTD 441
Qy      540 PSAVFDIHVVYVTTTETEMLDMSKPDGASEYVYHLVIESKHS--NHTSTYKAITLQGLIP 598
Db      442 PSAVTDIRVNIISTTEQLQEMQNTDASGYTHLVLESKGSIIIRNDSQKMITVGSILP 501
Qy      599 GTLYNITISPEVDHWGDPNSTAQYTRPSNVSNIDVSTNTTAAATLSQNFDDASPTYSYC 658
Db      502 GTLYNVTIPEVDIQISINSITQYTRPSSVSHLEVNTTTTAAIRKKNDAASASYAS 561
Qy      659 LILFKAGSSNAQVVT-DGIIDATVTELLIPGSSVYVELFAQVGDGKSLSPKRSFCT 717
Db      562 VLIKTDGSGNVTSNFKDPSI--LIPELIPGVSYYVKLITQVGDSTSLVPGMNLFC 618
Qy      718 DPASMASFDCGEVVPKEPALVLKWTCPGANAAGFELVSGAMNATLHSCSSENGTEYR 777
Db      619 EPEPVTSFRCGEVVPKEPALVLKACPFQMTTGPELGYRSDSMQNMTELENTSDDDTECR 678
Qy      778 TEVTVINFTSYNISITTVSCGKMAAPTRNTCTTGITDPPPDGSPNITSVSHSVKVF 837
Db      679 TEVAVLNFTSYNISITVSCGKMAAPTRNTCTTGITDPPPDGSPNITSVSHSVKVF 837
Qy      838 SGFASHGPIKAVAVILITTEGAGHPADVLKTYTDDPKKASADTVYVYLLRTEKGRSOS 897
Db      739 SGFASHGPIKAVAVILITTEGAGHPADVLKTYTDDPKKASADTVYVYLLRTEKGRSOS 897
Qy      898 LSEVLKYEIDVGNSTTIGYNGKLEPLGYSRACVAFNTITFHPQNGKIDGASVYSF 957
Db      799 LSEVLKYEIDVGNSTTIGYNGKLEPLGYSRACVAFNTITFHPQNGKIDGASVYSF 957
Qy      958 SRYSDAVSLPQDPGICGAVFGCIFGALVITVYGGFI FWRKRRKDAONNEVSFSQIKPK 1017
Db      859 SPYSEAVFLPQDPGICGAVFGCIFGALVITVYGGFI FWRKRRKDAONNEVSFSQIKPK 1017
Qy      1018 SKLIRVENFEAYFPKQADNSCGFAEYEDKLVGISQPKYAAALAEKGRNRYNNVLPY 1077
Db      919 SKLIRVENFEAYFPKQADNSCGFAEYEDKLVGISQPKYAAALAEKGRNRYNNVLPY 1077
Qy      1078 DISRVKLSVQTHSDTDYINANNYMPGYSKQDFIATQGPLPTLKDFFRMWMEKVVAAIIM 1137
Db      979 DISRVKLSVQTHSDTDYINANNYMPGYSKQDFIATQGPLPTLKDFFRMWMEKVVAAIIM 1137
Qy      1138 LTRKCEQGRKCEBYWPSKQADYDITVAMTSEIVLPEWTIRDFYKNIQTSSHPLRQ 1197
Db      1039 LTRKCEQGRKCEBYWPSKQADYDITVAMTSEIVLPEWTIRDFYKNIQTSSHPLRQ 1197
Qy      1198 FHTFSWPDHGVDPDTDLINFRYLVRDYMKSPPESPILVHCSAGVGTGFFIADIRLIY 1257
Db      1099 FHTFSWPDHGVDPDTDLINFRYLVRDYMKSPPESPILVHCSAGVGTGFFIADIRLIY 1257
Qy      1258 QIENENTADVYGIYVDLRMRHPLMVGOTEDQYVFLNQCVLDIVRSQKSKVDLIYQNTTAM 1317
Db      1159 QIENENTADVYGIYVDLRMRHPLMVGOTEDQYVFLNQCVLDIVRSQKSKVDLIYQNTTAM 1317
Qy      1318 TIYENLAPVTTFGKTNGYIA 1337
Db      1219 TIYENLAPVTTFGKTNGYIA 1337

RESULT 6
US-10-366-547-49
; Sequence 49, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE

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; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366,547
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1216
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-366-547-49

Query Match      64.0%; Score 4499.5; DB 15; Length 1216;
Best Local Similarity 67.1%; Pred. No. 7.3e-268;
Matches 900; Conservative 106; Mismatches 205; Indels 131; Gaps 10;

QY 1 MKPARARLPPSPGRLMLPLLLRLGOLCGGTPSPRPDSVATVATGNGITQ 60
DB 1 MKPARARTRTPSPGRLMLPLLLRLGQVAVTG----- 37
QY 61 ISSTASFKONGTGPQVETNTSEDESSGANDSLRTEQSGNGTDGASQKTPSSGTPS 120
DB 38 -----AAS 41
QY 121 PVFDKAVSISPTNVLITWKSNDTASERYVVKHENEKITTVHQPCNITGLRPT 180
DB 42 PVFDVEAVT-SPTSVVLTKHNDASATSEYKI-----NEGNTLRVTYVNGTSPNITGLSPAT 96
QY 181 SYVESITPGINETWGDPRVIVKITEPIPVSDLRVALTGVRKALSMKSGNCTASGRVLL 240
DB 97 SYFSTITLGVNNTSKRPYKNTITTEPWVSDQVAVIGVQALLAMSNANSTASYRMOI 156
QY 241 ESTGSHEILTQDRLQVNIISDLKPGVQVNIINPYLLQSNKTKGDPLETEGGLDASNTERSR 300
DB 157 -----VELTMS--SGGISDLKPGTHKSL--AVQSGNETQDMLWYTE----- 194
QY 301 ACSPTAPVHDESLVGPVDSGQGSQSDREVLVLVGERGRNATVYSSQANGTEGQPOAI 360
DB 195 -----GVSDPPSANDPSLTELLELTELKPDQVYVTTISQAADTEGQPNK 240
QY 361 ERTNIAIQVDTAVANISATSLTLIMKVSNDNESSNYTKIHVAGETSSNLNVEPRAY 420
DB 241 VEKTPDIQVSDIRAVNISDSNMTLWKSNNNSHASFYKIVVAGSGSINETVETIOAY 300
QY 421 IGLSSSTFYNTTCVGVLDIGETGFLQVHTPPVPVSDFRVTVSTTEIGLAMSSDAE 480
DB 301 IGLSSSTLYNTITVPLGQTAGIPGLQVTSPPRPSVDFRYTVNLSLEIGLAMSSDSE 360
QY 481 SFQMIITQAGANSRVEITTNOSIITIGLFPGTKYCFEIVPKPGVPGTEGASRTVCNRTVP 540
DB 361 SPEIFITQGSSEKRNNAATGDLSTYVNLKPGTSYQFEIIFRPGPVGTEGSPQTVVAGKDC 420
QY 541 SAVFDIHYVYVTTTMMWLDKSPDGASRYVHLVLESKHGNSHTSTYDKATLLOGLPGT 600
DB 421 SAVTDIRVVSSTTEILOEMQNTDSAGYVHLVLESNGSIKINSSQKMTTIGGLPGT 480
QY 601 LYNITISPEVHMGDPNSTAQYRPSNVSNIDVSTNTAATLSMOPNDASPRYSICLL 660
DB 481 LYNVITIFEVDOMESNSSITQYRPSNVSYIEVNTNTVGAIKWKLDAASASYSYVL 540
QY 661 IEKAGNSSNATQVYTDIGITDAVTEILPGSSYWEIF-----AQVGDGKISLEPGKRSF 715
DB 541 ILKADGDSNVTSRVD--IPSVTIPGLIPGVSEYKIFTKIRNTEVGENV---PGOKLF 594
QY 716 CTDPASMASPDCEVVPKPEPALVLMKTCPPGANAGPELEVSSGANNATHLESCESENGTE 775
DB 595 CMEPQVDSLCEVVPKPEPALVLMKACPPGNNSGFELGVNSDADAMNTHLENCTLDNTE 654
QY 776 YRTEVTVNFSSTYSYISITTVSCGMAAPTNCTCTGTDPDPDGSNITTSVSHSVKV 835
DB 655 CRTETVTVNFSSTYNISIAITSCGKMLPTOSTCTGTGTDPPPDGSPNITTSVSHSVKV 714
QY 836 KFSGEASHGPIKAVAVILTTGEAGHPADVLKTYTDDFKKGSADTVVTVLIRTEKGRS 895

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DB 715 KFSGEASHGPIKAVAVILTTGEAGHPSTDLKTYTEDEPKKGSADTVVTVLIRTEKGRS 774
QY 896 QSLSEVLKYEIDVGNESITLLGYNGKLEPLGSYACVAGFTNITFHPONKELIDGASYSV 955
DB 775 QGLSEALNVEIDVGNOSTLLGYNGRLEPLGSYACVAGFTNITYNINQNDGLINGDSYV 834
QY 956 SFSRSYSDAVSLPDPBGVTCGAVFGCIRGALVITVGGIFEMRRKKRDKAKNNEVSFSQIKP 1015
DB 835 SFSFSYSEAVSLPDPBGVTCGAVFGCIRGALVIVAVGFIEMRRKKRDKAKNNEVSFSQIKP 894
QY 1016 KKSILIRYENFEAYFKQQAQNSNCGFAEYEDLKVGISQPKYAEIAENRGRKRVNVL 1075
DB 895 KKSILIRYENFEAYFKQQAQNSNCGFAEYEDLKVGISQPKYAEIAENRGRKRVNVL 954
QY 1076 PYDISRVKLSVQTHSTDDYINANNYPGYSKQPIATQGPLNTLKQFWMVEKKNVYAI 1135
DB 955 PYDISRVKLSVQTHSTDDYINANNYPGYSKQPIATQGPLNTLKQFWMVEKKNVYAI 1014
QY 1136 IMLTKVBOGRTKCEEYWPSSKQADYGDITVAMTSEIVLEPMTIRDPYVKNITQSSSHP 1195
DB 1015 VMLTKVBOGRTKCEEYWPSSKQADYGDITVAMTSEIVLEPMTIRDPYVKNITQSSSHP 1074
QY 1196 RQFHTSPDHGVBDTDLINFRYLVRYDMKOSPSPSPILVHCSAGVGTGFIAIDRL 1255
DB 1075 RQFHTSPDHGVBDTDLINFRYLVRYDMKQIPSPSPILVHCSAGVGTGFIAIDRL 1134
QY 1256 IYQIENENTVDYGVIVDLMHRPLMVTQEDQVFLNQCVLDIVRSQKSVLDIYQNTT 1315
DB 1135 IYQIENENTVDYGVIVDLMHRPLMVTQEDQVFLNQCVLDIVRSQKSVLDIYQNTT 1194
QY 1316 AMTIYENIAPVTPGKTNGYIA 1337
DB 1195 AMTIYENIAPVTPGKTNGYIA 1216

RESULT 7
US-10-723-606-3
; Sequence 3, Application US/10723606
; Publication No. US20040161821A1
; GENERAL INFORMATION:
; APPLICANT: Palke-Hamblin, Helena L.
; TITLE OF INVENTION: DEP-1 RECEPTOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE INTERACTING PROTEINS
; FILE REFERENCE: 200125.447
; CURRENT APPLICATION NUMBER: US/10/723,606
; CURRENT FILING DATE: 2003-11-26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-606-3

Query Match      25.8%; Score 1811; DB 16; Length 341;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 997 RKKRKDAKNNNEVSFSQIKPKKSKLIRVENFEAYFKQQAQNSNCGFAEYEDLKVGISQ 1056
DB 1 RKKRKDAKNNNEVSFSQIKPKKSKLIRVENFEAYFKQQAQNSNCGFAEYEDLKVGISQ 60
QY 1057 KYAAELAEENRGRKRVNVL PYDISRVKLSVQTHSTDDYINANNYPGYSKQPIATQGPL 1116
DB 61 KYAAELAEENRGRKRVNVL PYDISRVKLSVQTHSTDDYINANNYPGYSKQPIATQGPL 120
QY 1117 PNTLKQFWMVEKKNVYAIMLTKVBOGRTKCEEYWPSSKQADYGDITVAMTSEIVLE 1176
DB 121 PNTLKQFWMVEKKNVYAIMLTKVBOGRTKCEEYWPSSKQADYGDITVAMTSEIVLE 180

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QY 123 FDIKAVSISPTNVLITWMSNDTPAASEYKVVGHKHENETTIVVHQPMCNITGLPAPSY 182
Db 759 FDHEVITIKANKNFQTSIP-----KSENE-----CVFQVLPGRLY 796
QY 183 VESITPGIG---NETWGDPRVIKYTEPIPVSDLRVALTGVKKAALSMNSNGTASCXY 238
Db 797 SVTWTTKGQYEANEO-GNGRTI-----PEPYKDLTLNRSTEDJLHWMSGANG----- 844
QY 239 LLEBSGHE-ELTODSRL-----QVNIDLKPGVOY---NINPYLLQSNKT 280
Db 845 --DVDQYEIQLLFNDMKVFPFPHLVNTATEBRFTSLTPGRYKILVLTISGDVOOSAFI 901
QY 281 KG-----DPLG-----TEGGIDAN-----TERSRAGSPAPAPHDSL 313
Db 902 EGFVTPSAVKNIHISPNQATDLSLTWNMTBPGGDVDVSUYVASFRHSQKDSQITPPH--- 957
QY 314 VGPVDPSSGOOSRDTEVLLVGLPEPTRYNATVYSQANGTEGQPOAIBERTVAIOVFDVT 373
Db 958 -----VFHFTFRLREAEQOQIMAS--VGSGLNQINQVGRITVPASVQGI 1004
QY 374 AVN-ISATSLTLIMKVSNDNESSNYYKIHVAGEFTDSSNLNVSEPPA-----VITGL 424
Db 1003 ADNMAVSSYSLIVSMOKAGVAAE--RYDILLTLENGILLRMTSEBATTIKOHKFEDLTGPK 1058
QY 425 RRSFTYNTITVCVPGDIBETPGFLQVHPRPVPSDFPRTVVUSTTIGLAWSSHDESFGM 484
Db 1060 K---YKIQILTVSGGLPSKEAQOTGRTPAAVTLDRITENSTRHSFRMTASBEELSWY 1116
QY 485 HI---TOEAGNSRVEI--TTNQSIIIGGLFPCTKYCFEIVPAGPMTGEGASRTVCNRTVP 540
Db 1116 NIFLNPNGNIQERQVDPVIVGSPFQNLQSRMTKMYLVH--SGELSNESFIRGRITVP 1177
QY 541 SAVEDIHVVVYTTLE-MWLDWKSPPGABEYVYHVLVIESKHGSHNTSTYDKAIT--LOGL 596

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RESULT 9
US-09-909-567B--54
; Sequence 54, Application US/09909567B
; Publication No. US2003002257A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto A.
; APPLICANT: Nair, Manoj
; APPLICANT: Chen, Selvu
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0214
; CURRENT APPLICATION NUMBER: US/09/909,567B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21
;

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NUMBER OF SEQ ID NOS: 56
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 54
 LENGTH: 1997
 TYPE: PRF
 ORGANISM: Homo sapien
 US-09-909-567B-54

Query Match 17.7%; Score 1241; DB 10; Length 1997;
 Best Local Similarity 29.6%; Pred. No. 5.1e-67;
 Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

123 FDIKAVISPTNVLTKWNSDNTAASEYKVVGHKMEKNTITVHQPMCNITGLPATS 182
 759 FDHYEVTIKNNKNIQTKSIP-----KSENE-----CVFQVLPGRLY 796
 183 VRSITGIG-----NEWGDPRIYKITEPIPSDLRVALTGKKAALMSNGNGTASCRV 238
 797 SVTVTKSGQYEANRQ-GNGRTI-----PEPVKDLILNRSTEDLHVWSGANG----- 844
 239 LLESIGSHE--ELTODSRL-----OVNISDLKPGVOY-----NINPYLLQSKNT 280
 845 ---DVDQYEIQLLFNDMKYFPFHLVNTATETRFSTLTGROYKILVLTISGDVQOSAFI 901
 281 KG-----DPLG-----TEGLDASN-----TERSRAQSPTAPVHDSL 313
 902 EGFTPSAVKNIHISNGATDSLTVWMTFGGDVDISTVSARHSGKVDSCITIPKH----- 957
 314 VGPVDPSSGQSRDTEVLVGLPEGRVNAITYSOANGTEGQPAIEFRNALQVDPVT 373
 958 -----VEHTHRLHASEQYOIMIAS--VSGSLKNOQINVGRTVPASVQGI 1002
 374 AVN-ISAFTSLTLMKVDNNESSNYTKIHVAGETDSSNLNVEBRA-----VIRPL 424
 1003 ADNAVSSYSLIWSQKAGAVAE--RYDILLTENGILLRNTSEPAITKQKHEDLTPGK 1059
 425 RSTSTYNTVCPVLDIGETPGFLQVHPVPVSPFRVTVSTTEIGLAMSHDASESQM 484
 1060 K---YKQILTVSGSLFSKEAQTGRVPAVTLRLITENSTRILSPFRMASEBELSWY 1115
 485 HT---TOGAGNSRVEI--TTNOSIIIGGLPGTKYCFEIVPKGPGTEGASRTVCNRTVP 540
 1116 NIFLVNPGNIQERQVDPVIVGFSFOULQCRMTKMTIVH--SGELSNESFIRGRTVP 1173
 541 SAVFDIHVVYVTTT--MWLDWKSPPDGAEEVYHVLIESKHSNHTSTYDKAIT--LOGL 596
 1174 ASVSHLRGNSNRNTDLSLWFNWSPASGDPDF-YELLIVPNNGTKKEMKDXDLTEMRFGSL 1232
 597 IPGTLNITISPEVDHWGDPNSTAQYTR-----PSNVSNIDVSTNTTAATL---SWQN 647
 1233 VPGKTYLVW---VTHSGDLSNKTATASRTAPSPSLMSFADIANSTSLATITWKGPPMTD 1289
 648 FDDASPTV---SYCLLIEKAGNSNATQVTDIGITDATTVELIPGSSYVEIPIAQVGDG 704
 1290 YNDFELQWLPRDALTFVFNPNNRKSEGRIVG-----LRPGNSYQNNVATVSGDS 1339
 705 IKSL-EPKRSFCTDPSMASFDCVVPKEPALVLKWTCPGANAGAELEEVSSGANNAT 763
 1340 WKTYSKPIFGSVRKPKDKIOMLHCR-PONSTAIACSWIPPOSDDGYISIE-----CR 1390
 764 HLESCESENGETEYRTEVYLNFE-----STSYNISITTVSCGKMAAPRNTCTTGITDPP 818
 1391 KMDIOVEVFSKLEKESKSLNIMMLVPHKRYLVSIKVQASAGMTSEVEDSTTIDRPP 1450
 819 PDGSPNI-----TSVSHSVK--VKSGFEASHGPIKAVAILTTG-----EAGHP 862
 1451 P--PPIHVKNEKOVLISKSSINFVNCMSWFDSTNGAKYFTVVVREADGSDDELKPPDQHP 1508
 863 SADVLKITYDPPKKGASDTTYTYLIRTBKGRSQSLSEVLKYEIDVNESTTIG----- 916
 1509 LPSTYLEKHNASIVYQNTY--FASKCAENPNSNKS-----FNIKLGAEMESIGGKCDPT 1562
 917 ---YVNGKLEPLGSRACVAGFTNITTFHPQKGLIDGAEVYVSR--YDA-VSLP--- 967

1563 QOKRDEGLKPHHTYRISIRAFTO-----LPD--EDIKETKPLYSDTSPSLPITT 1611
 968 -QDPGVIGAVFGCIPGALVI---VTVGFIWFRK--RDKAKNNEVSFSQIKP----- 1015
 1612 ESEP--LFGAIEGVASGIFLIGMLVAVALLICQKVSHERERSALSTRDRDPLSVHL 1669
 1016 -----KSKKLRVNFEAFYFKQOADSNGCAEYEDLKVGISQPKYAAELANRG 1067
 1670 NLGQKRNKRTISCPKINQFEGHEFKLOADSNVYLLSKEKEELKQVGRQOSCDILLPNRG 1729
 1068 KNRVNVLPYDISHVLS--VQTHSTDDYINANVWPGHSHKDDFATQGPPLTKDPFWM 1126
 1730 KNRVNVLPYATATVKLSNVDDECSYINASYIPGNFRREYIVYQGPLPGTKDPMKA 1789
 1127 VMEKOVTAIIMLIKVEQGTKEEYWPSSKO-AQVYGDITVAMTSEIVLDEWITRDETVK 1185
 1790 VMEQNVHNIWVWTCQVEKGRVKCDHWYPADQDSIYDGLILOMLSESVLPBMTIRREKIC 1849
 1186 NIOSESHP--ROPHFTSWPDHGVDPDTLLIMPRVYRPMYKQSPRESFIVHCSAGVG 1244
 1850 GEEQLDHRLIRHFHYWPDHGVPEYTSGLIOPRTVRYINRSPAGFTVHCSAGVG 1909
 1245 RTGTFIADRLIYOIENENTVDVYGIYDLMRMRPLAVQTEDQYVFLNQCLDIVERQKD 1304
 1910 RTGTFIADRLIQLQDSKSDVDIYGAVHDLRLRHVMVQECQYVYLHCQVRDVLARKL 1969
 1305 SKVDLITQNTTANTTIENLAP 1325
 1970 RS-----EQENPLPEIYENVP 1986

RESULT 10
 US-10-408-765A-2135
 Sequence 2135, Application US/10408765A
 Publication No. US20040101874A1
 GENERAL INFORMATION:
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Faby, Boia D.
 APPLICANT: Zhang, Bing
 APPLICANT: Gibson, Bradford W.
 APPLICANT: Taylor, Steven W.
 APPLICANT: Glenn, Gary M.
 APPLICANT: Wainock, Dale E.
 TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 FILE REFERENCE: 660088 465
 CURRENT APPLICATION NUMBER: US/10/408, 765A
 CURRENT FILING DATE: 2003-04-04
 NUMBER OF SEQ ID NOS: 3077
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2135
 LENGTH: 1997
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-10-408-765A-2135

Query Match 17.7%; Score 1241; DB 16; Length 1997;
 Best Local Similarity 29.6%; Pred. No. 5.1e-67;
 Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

123 FDIKAVISPTNVLTKWNSDNTAASEYKVVGHKMEKNTITVHQPMCNITGLPATS 182
 759 FDHYEVTIKNNKNIQTKSIP-----KSENE-----CVFQVLPGRLY 796
 183 VRSITGIG-----NEWGDPRIYKITEPIPSDLRVALTGKKAALMSNGNGTASCRV 238
 797 SVTVTKSGQYEANRQ-GNGRTI-----PEPVKDLILNRSTEDLHVWSGANG----- 844
 239 LLESIGSHE--ELTODSRL-----OVNISDLKPGVOY-----NINPYLLQSKNT 280
 845 ---DVDQYEIQLLFNDMKYFPFHLVNTATETRFSTLTGROYKILVLTISGDVQOSAFI 901

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Qy 281 KG-----DPLG-----TEGLDASN-----TERSAAGSPTAVHDESL 313
Db 902 EGFVPSAVKNIHISPNGATDSLTVMTPPGGGDVDSYVSAFRHSQKDSQTIPIKH----- 957
Qy 314 VGPVDPSSGQGSRDTEVLVLGLEPCTRYNATVYSGAANGTEGQPOALEFFRTNAIQVDPVT 373
Db 958 -----VFEHTFHRLEAGEQYQIMIAS--VSGSLKQINIVVGRTPVPSVQCVI 1002
Qy 374 AVN-ISAATSLTLIKVSDNESSNNTYKIHVAGETDSSNLNVSEBRA-----VLPGL 424
Db 1003 ADNAVSSYSLIVSMQKAGVAE--RYDILLTENGILLRNTSEPAATTKQKHFEDLTPGK 1059
Qy 425 RSTFTYNTVCPVLGLEGTGFLQVHTPPVPVSDFRVTAVSTTEIGLAWSHDAESFQM 484
Db 1060 K-----YKIQILTVSGGLFSKQAQTEGRTPVAAVDLRTENSTRLHSRWASGEELSMY 1115
Qy 485 HI---TOEGAGNSRVEI-TTNQSIIGGLPQTKYCFEIVKPGNGTEGASRTVCNRTVP 540
Db 1116 NIFLYNPQGNLQEBRAQVDPVLQSFQNLQGRMYKVIYTH--SGELSNESFIFGRTPV 1173
Qy 541 SAVPDIHVYVYTTTE-WMLDKKSPDGASEVYVYHLYIESKHSNHTSTYDAIT---LOGL 596
Db 1174 ASVSHLGNSNNTTDSLMFNMSPASGDPE-YELLVNPNGTKKENMKDKDLTEWRFQGL 1232
Qy 597 IPGTLVNTTISPEVDHVGDNSTAQYTR-----PSNVSNIDVSTNTTAATL---SWQN 647
Db 1233 VPGKRYVLWV---VTHSGDSLNTKYAESRTAPSPSPSLMSPADIANTSLAITMKGPBMTD 1269
Qy 648 PDDASPTY---SYCLLIEKAGNSSNATQVTDIGITDATTETELIPGSSYVEIFAQVGDG 704
Db 1290 YNDELEQLPDPALTLVFNPYNNRKSEGRIVYG-----LBRGSRYSQNVAKTVSGDS 1339
Qy 705 IKSL-EPBRKSFCDPDPMASAFDCEVKEPALVLYAKTCPPGANAAGFLLEVSSGAMNAT 763
Db 1340 WKYTSKPLFGSVKRPDKIQNLHCR-PONSTALACSMIPPSDPEVYSIE-----CR 1390
Qy 764 HLESCESENGETEYETVYLNLF-----STSYNISITTVSCGKMAAPTNTCTGTIDPPP 818
Db 1391 KMDQVEVEFSRKLKESKSLNIMLVPHIKRYLVSLKYQGSAGMTBSVVDSTITIMIDRRP 1450
Qy 819 PDGSPNT-----TSVSHSVK--VKFSGFASHPKIAVAVILTTG-----EAGHP 862
Db 1451 P--PPHIRVNEKDVYLISKSSINFVNCMSFSDTNGAVKCYFVVVREADSGDELKPEQHP 1508
Qy 863 SADVLAKTYDDPKKASDTYVYLYLIRTEKGRSOSLSVLKCYLDVGNESITLG----- 916
Db 1509 LPSYLEYRHNASIRYQTNV--FASKCAENPNNSKS-----FNIKLAGEMESLGKCDPT 1562
Qy 917 ---YUNGKLEPLGSYRACVAGFTNITFHPKGLIDGASVVSFSR--YSDA-VSLP--- 967
Db 1563 QQKCDGFLKPHTRVIRISIRAFQ-----LFD--EDLKEFTKPLYSDTFFSLPITTT 1611
Qy 968 -QDBGVICGAVFGCIFGALVI---VTYGGFIEMRK--RKDAKNEVSFSQIKP----- 1015
Db 1612 ESEB--LEGALEGVSAGLFLIGMLVAVVALLICROKVGHERPSARLISIRDRRLSVHL 1669
Qy 1016 -----KSKLIRVENFEAFYKKQADSNCGFAEEFEDLKYGISPKYAAELAEKRG 1067
Db 1670 NLGQGNKRTKSPCKINQFEGHFMKLQADSNYLLSKYEELKLDVGRNOSCDIALLPENRG 1729
Qy 1068 KNRNVNVLPLYDISVYKLS-YQTHSTDYINANVMPGVHSGKDOFATOGPLPNTLKDFPRM 1126
Db 1730 KNRNNNLLPYDATVYKLSNVDDDDPCSDIYNASTYIPGNFRREYIVTQGPLPGETDKDFPKM 1789
Qy 1127 VMEKNVYAIIMLTVCVQGRKCEYWPBSQ-ADYGDITVAMTSEIVLPMTIRDFTVK 1185
Db 1790 VMEQNVNHIIVMTQCVKEKGVKCDHYMPADQDSLYGDLILQWSESVLPMTIRREFKIC 1849
Qy 1186 NIQTSSEHPL-RQHFHTSWPHGVPTDILLINRYLVYVDYMKQSPSPSLVYHCSAGVG 1244
Db 1850 GEEQLDARLIRHFRHYTVMPDHGVETQSLIQFRYRTVYINRSFGAGPTVYHCSAGVG 1909
Qy 1245 RTGFIAIDRLIYQIENENTVDVYGIYVDLWHRPLWQTEQVYFLNQCVLDIRSQKD 1304

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Db 1910 RTGFIAIDRLIQLQDSKSDSDIYGAVHDLRHRHVWQTECOYVYLHQCVRDVLRARL 1969
Qy 1305 SKVDLIYQNTAMTAYENLAP 1325
Db 1970 RS---EQENLFPFIYENVNP 1986

RESULT 11
US-10-497-692-4
; Sequence 4, Application US/10497692
; Publication No. US2005004056A1
; GENERAL INFORMATION:
; APPLICANT: Weise, Martin
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Fritsch, Rudiger
; APPLICANT: Hader, Thomas
; APPLICANT: Broemer, Gunter
; APPLICANT: Steuernagel, Arnd
; TITLE OF INVENTION: PPIID, Tec protein tyrosine kinase and EDPp homologous proteins
; TITLE OF INVENTION: involved in the regulation of energy homeostasis
; FILE REFERENCE: 2923-632
; CURRENT APPLICATION NUMBER: US/10/497,692
; PRIOR APPLICATION NUMBER: PCT/EP02/13744
; PRIOR FILING DATE: 2004-06-04
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: EP 01 000 010.5
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EP 01 129 138.2
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: EP 01 128 844.6
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-692-4

Query Match 17.7%; Score 1241; DB 16; Length 1997;
Best Local Similarity 29.6%; Pred. No. 5.1e-67;
Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

Qy 123 FDIKAVSISPTNVLITKMSNDTASVYKVKHKNKMKETITVHQPWCNTIGLRPATSY 182
Db 759 FDHYEVITIKKNKNDPIQTKSIP-----KSENE-----CVFQVLVGRLY 796
Qy 183 VFSITPGIG---NETGDDPRVIVKITEPIPVSDLRVALTGVRAKALSMNGNSTASCRV 238
Db 797 SVYTTTSGQYEANBQ-GNGRTI-----PEPVKDLTLRNSTEDLHTWMSGANG----- 844
Qy 239 LLESIGSHE-ELTQDSRL-----QVNISDLKPGVQY-----NINPYLLQSNKT 280
Db 845 ---DVDQYEQLLFPNDKMFPPFPFLVNTATERYFTSLTPGQYKILVLTISGVOQSFAFI 901
Qy 281 KG-----DPLG-----TEGLDASN-----TERSAAGSPTAVHDESL 313
Db 902 EGFVPSAVKNIHISPGATDSLTVMTPPGGGDVDSYVSAFRHSQKDSQTIPIKH----- 957
Qy 314 VGPVDPSSGQGSRDTEVLVLGLEPCTRYNATVYSGAANGTEGQPOALEFFRTNAIQVDPVT 373
Db 958 -----VFEHTFHRLEAGEQYQIMIAS--VSGSLKQINIVVGRTPVPSVQCVI 1002
Qy 374 AVN-ISAATSLTLIKVSDNESSNNTYKIHVAGETDSSNLNVSEBRA-----VLPGL 424
Db 1003 ADNAVSSYSLIVSMQKAGVAE--RYDILLTENGILLRNTSEPAATTKQKHFEDLTPGK 1059
Qy 425 RSTFTYNTVCPVLGLEGTGFLQVHTPPVPVSDFRVTAVSTTEIGLAWSHDAESFQM 484
Db 1060 K-----YKIQILTVSGGLFSKQAQTEGRTPVAAVDLRTENSTRLHSRWASGEELSMY 1115
Qy 485 HI---TOEGAGNSRVEI-TTNQSIIGGLPQTKYCFEIVKPGNGTEGASRTVCNRTVP 540

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Db      1116 NIFLYNPDGMLQSRQAQVPLVQSFSPQNLQGRMYKAVLYTH--SGELSNESIPIGRITP 1173
Qy      541 SAYPDHVVVYVTTT-MWLDKSPDASAEVYHVLVIESKSGNSHTSTYDKAIT--LOGI 596
Db      1174 ASVSHLGSNRNNTTDSLMFNWSPASGDPDF-YELIYNPNGTCKEKKWKDKDLEMFQGL 1232
Qy      597 IPGTLVNTISPEVDHWGDPNSTAQYTR-----PSNVSIDVSTNTTAATL--SMON 647
Db      1233 VPKRKVLYWY---VTHSGDLNKNVTAESRTAPSPSLMSFADTANTSLIITWKGPDPWTD 1289
Qy      648 FDDASPTY---SYCLLEKAGNSNATQVVTDTGTDATVTELIPISSYVIEFAQVGDG 704
Db      1290 YNDFELQWLPDALTFFNPNYNNRKSSEGRIVYG-----LRPGRSQFQVNTKVSQGS 1339
Qy      705 IKSL-EPGRKSFCTDPASMASPDCEVVPKEPALVLTWTPCPGANAGFELEVSQAMNAT 763
Db      1340 WKTYSKPIGSAVTKKDKIQNLHCR-PQNSTALACSWIPDSDPDGYSIE-----CR 1390
Qy      764 HLESCSENGTEYRTVYTLNF-----STSYNISITTVSCGKMAAPTRATCTGTDP 818
Db      1391 KMTQVEFSRKLKEKSKLNLIMLVPHKRYLVSIVQAGMTSEVVEDSTITMIDRPP 1450
Qy      819 PDSPNI-----TSVSHSVK--VKSGPEASHGPICAVAVILTTG-----EAGH 862
Db      1451 P-PPHIRVNEKDVILASKSINFETVNCWSFSDTNGAVKYFVVVHEADGSDDELKPEQGP 1508
Qy      863 SADVLKTYDDDFKGSADTYVYTLIRTEKGRSQSSEVLKKEIDVGNSTILG----- 916
Db      1509 LSVYLEYRNASIRVQVNY--FASKCANPNNSNS--FNILKGMESLGSKDPT 1562
Qy      917 ---YNGKLEPIGSAVCAVGFNTITFHPQNKGLIDGASVVSFSR--YSDA-VSLP--- 967
Db      1563 QOKFCGPIKPHATYASIRAFIQ-----LFD--EDLKEFTKPIYSDTFSLPIT 1611
Qy      968 -ODPGVIGAVGECIFGALVI---VTYGGFIEMRK--RKDAKNEVSFSQIKP----- 1015
Db      1612 ESEF--LFGALIEGVSAGLFLIGMLVAVALLCRKQVSHGRERPARLSIRDRPLSVHL 1669
Qy      1016 -----KSKLIRVENFEAFYFKQADNSCGFAEEYEDLVISOPKTAABLAENRG 1067
Db      1670 NLQKGNRKTCSPKIKNGEHPMLQADSNVLLSKYELKDVGRNOSCDIALPEKRG 1729
Qy      1068 KRRYNNVLPYDISRYKLS-VQTHSTDDYINANYPGHSKDFIATQGPLFNILKDFWRM 1126
Db      1730 KRRYNNILPYDATRYKLSNVDDPCSDIYNASYIPGNFRREYIVTQGPLGTQDFFWK 1789
Qy      1127 VKEKNVYAILMLTKCEQGRKCEBYWPSKO-AQDYGDITVAMTSEIYLPMTIRDPYVK 1185
Db      1790 VWEQVNHNIWVYTCVEKGRVCKDHWPADODSLYTGDLIQMLSESVLPMTIRREFKIC 1849
Qy      1186 NIQISESHPL-RQHFITSMPDHGVPTDULLINFRYLVADYMKQSPESPILVHCSAGVG 1244
Db      1850 GEEQDARHLIRHFHYTWPDPHGVETQSLIQFRTVADYINSPGAPFVHCSAGVG 1909
Qy      1245 RTGFIALDLILOYENENTVYVIGVYDLMRHPMLQTEDQYVFNOCYLDIVRSOKD 1304
Db      1910 RIGFIALDRILIQDSDKSDSDIYGAVHDLRLHVMVQTECOYVYVHOCVAVLRAKRL 1969
Qy      1305 SKVDLIYONTTAMTIYENTLAP 1325
Db      1970 RS---EQENPLPIYENVP 1986

RESULT 12
US-10-497-692-14
; Sequence 14, Application US/10497692
; Publication No. US20050004056A1
; GENERAL INFORMATION:
; APPLICANT: Meise, Martin
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Fritsch, Rüdiger
; APPLICANT: Hader, Thomas

; APPLICANT: Bromner, Gunter
; APPLICANT: Steuerragel, Arnd
; TITLE OF INVENTION: PPIID, Tec protein tyrosine kinase and EDP homologous proteins
; TITLE OF INVENTION: Involved in the regulation of energy homeostasis
; FILE REFERENCE: 2923-632
; CURRENT APPLICATION NUMBER: US/10/497,692
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: PCT/EP02/13744
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: EP 01 000 010.5
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EP 01 129 138.2
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: EP 01 128 844.6
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 1450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-692-14

Query Match      17.5%; Score 1230; DB 16; Length 1450;
Best Local Similarity 29.3%; Pred. No. 1.5e-66;
Matches 390; Conservative 197; Mismatches 495; Indels 250; Gaps 53;

Qy      125 IKAVISPT---NVILTKSNPTAASEYRYVVKH-----KMEKTIIVVHOP 169
Db      216 VQGVSVNSARSIDLRYVSWHATGDFDHYEVTKIKNNNFQTSKIPSENE----- 266
Qy      170 WCNTIGRPATSVYFSTIPGIG---NETWGDRLVKVITEPIPVGDDKALTVKAKAL 225
Db      267 -CVVQVLVPGRLSVYVTTYSGGYEAHQ-GNGRTI---PEPVDLTLRNSTEDLHV 319
Qy      226 SMSNGNGTASCRLVLESIGSHE--ELTODSRL-----QVNIISDKPGVOY--- 268
Db      320 TWGANG-----DVDQYEIQLFNDMKVPPPHLVNVAIEYFTSLTPRQYKILV 370
Qy      269 -NINPYLIQNNKTG-----DPLG-----TBGGLDASN-----TERSR 300
Db      371 LTISGVDQSAFIEGFTVPASVAKNIHISPQATDSLTVMWTPGGGVDSDTVSAPFHSOK 430
Qy      301 AGSPFAVHESLVGVPDPSGQSSRDTEYLVLGEPGRYNAVTVYVQANGREGQPAI 360
Db      431 VDQGIPIKH-----VFETFRHLRAGQIQIMAS--VSGSLKQIIV 471
Qy      361 EPTTNAIOYFDVTAVN-ISAATSLILWKVSDNESSNTYTKIHVAGETDSNINVSEPPA 419
Db      472 VGRTPASVQGVYADNAVSSYSLIVSMQKAGVAB--RYDILLTENGILLRNSEPAT 528
Qy      420 -----VTPGRSSTFNITVCPYLDIEGTPGLQVHTPPVPVSDPRVTVSTTEIG 471
Db      529 TKQHKEDLLPGKK---YKIQLTVVSGGLFSEKAQTEGRVPAATDLIRITENSTRHS 584
Qy      472 LAWSHDAESFQWHL---TOEGAGNSRVEI--TTNOSIIIGGLFPGTKYCFEIVPGPNGT 527
Db      585 FRNTASBEGELSMWNIPLVNDGNLQERAVUDLVQSFQNLQGRMYKAVLYTH--SGE 642
Qy      528 EGASRTVCNRTVPASAVFDIHVVYVTTT-MWLDKSPDASAEVYHVLVIESKSGNSHTST 586
Db      643 LSNESFIFGRTPASVSHLRGSRNNTTDSLMFNWSPASGDPDF-YELIYNPNGTCKEKNW 701
Qy      587 YDKAIT---LOGIIPGTLVNTISPEVDHWGDPNSTAQYTR-----PSNVSIDVSTNT 638
Db      702 KQKDLTEMFQGLVGRKTVLYWY---VTHSGLSKNVTAESRTAPSPSLMSFADTANTSL 758
Qy      639 TAATL---SWQNFDDASPTY---SYCLLEKAGNSNATQVVTDTGTDATVTELIPIGS 691
Db      759 LAITWKGPDPWTDYNDFELQWLPDALTFFNPNYNNRKSSEGRIVYG-----LRPGR 808
Qy      692 SYTVIEFAQVGDIGISL-EPGRKSFCTDPASMASPDCEVVPKEPALVLTWTPCPGANAGF 750

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Db      809 SYCFNFKVSGDWMKTSKPIFGSVTRPKDIONLHCR-PONSTAIACSWIPDSDPDGY 867
Qy      751 ELEYSAGMANNATHLESCESSNGTEYREYVLYNF-----STSVNISTTVSCGMMAPT 805
Db      868 SIE-----CRKADIOEVEFSRKLKESKSLNMLVPHKRYIVSTIKVOSAGTSEBV 919
Qy      806 RNTCTTGITDPPPGSGPNI-----TSVSHSVK-VKFSGFSAHSPIKAYAVILTTG 857
Db      920 EDSTITMTDRPPP--PHIRVNEKDVILSKSSINFNTNCSFSTPNNAVKFYTVVMEA 977
Qy      858 -----EAGHPASADVLKTYTDDPKKASDPTVYTYLIRTEBKRSQSLSEVLKYEIDVG 909
Db      978 DGSDELKEQOQHPLPSYLEYRHNASIRVYQNTY--FASKCAENPNSNKS-----FNILKG 1031
Qy      910 NESTTLG-----YNGKLEPLGSYRACVAGTNTTTHPQNGKILDGAEYSYSPR- 959
Db      1032 AEMESLGGKCDPTQOKFCDDGLPKPTAYRISRATQ-----LFD--EDLKEFTKP 1080
Qy      960 -YSDA-VSLP-----ODPGVICGAVGCIFGALVI---VTVGGFIFMRK---RKDAKNE 1007
Db      1081 LYSDFEFLPITTESEP--LFGALIGVSAGLFLIGMLVAVALLICRQVGHGRERSAR 1138
Qy      1008 VSPFOIKP-----KSKLIRENFEAFYKKQADNSCGFAEYEDLKLVGIS 1054
Db      1139 LSIHRDRPLSVHNLGQKGNKRTSCPIKINQFEGHFMLQADSNYLSKEYEELKDVGRN 1198
Qy      1055 QPKAAELAEHRGKRRYNNVL.PYDISRYKLS-VQHSRDDYINANMYGHSKDFITQ 1113
Db      1199 QSCDIALPERGKRRYNNILPYDATRYKLSNVDDPCSDYINASYIGANNFRREYITQ 1258
Qy      1114 GPLPNTLKDFFRMWMEKNVVAIIMLTKECEQRTKCESEWPSKQ-AQDYGITVAMTSEI 1172
Db      1259 GPLGCTKDDFKMWEQONVHNIWMTQCEVKRGVCHHWPRADQSLYGGDLILQMSSES 1318
Qy      1173 VLPEWTRDFTVKNQIQTSESHPL-RQHFETSPMDHGVDTTDLINFRYLVADYKQSP 1231
Db      1319 VLPEWTRDFTVKNQIQTSESHPL-RQHFETSPMDHGVDTTDLINFRYLVADYKQSP 1378
Qy      1232 ESPLVHNSAGVGRGTIAIDRLIYQIENENTVUVGIYVDLRHRLMOTEOGYFL 1291
Db      1379 AGPVTWHCSAGVGRGTIALDRILQDLSKDSVDIYGAVDRLRHVMVOTECQYVL 1438
Qy      1292 NOCVLDIVRSOK 1303
Db      1439 HQCVRDVLRARK 1450

RESULT 13
US-10-245-539-2
: Sequence 2, Application US/10245539
: Publication No. US20030077638A1
: GENERAL INFORMATION:
: APPLICANT: Logan, Thomas Joseph
: TITLE OF INVENTION: MID 4460, A HUMAN TYROSINE PHOSPHATASE
: FILE REFERENCE: MP101-155P1RM
: CURRENT APPLICATION NUMBER: US/10/245,539
: PRIOR FILING DATE: 2002-12-05
: PRIOR APPLICATION NUMBER: 60/323,018
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 1118
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-245-539-2

Query Match      16.1%; Score 1130; DB 14; Length 1118;
Best Local Similarity 25.9%; Pred. No. 1.5e-60;
Matches 354; Conservative 181; Mismatches 453; Indels 380; Gaps 40;

Qy      8 ARLPRSPG-----LRWALPLLLLLRLGLIACGCTPSPIDPSPVATVAT 53

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Db      25 ARAPAPNGRLIVETQTTSSISLSMEVP-----DGLDS--QNSVWVOCT 68
Qy      54 GENGITQISAESEFHKQNGCTPOVETNTSEDESSGA--NDSLRTPEGSNGTDAQ 111
Db      69 GGGTTERNT-----TATNTVDDLGRPSLYTGSVWEKQDVNSVGT-- 112
Qy      112 KTPSTGSPVPIKAVISPTVILTWKSNDAASEK-VYVGHKENEK--TITVHQ 168
Db      113 -VTTATAPNVRNLRVBAQNTSSIALTWVEVDGDPQNSTYGVYTGDDGAGRSTAH- 170
Qy      169 PWCNIT--GLRPATSYVFSITPIGNETWGDPRVIKYTEBIPVSLDLVALTGVKALS 226
Db      171 --TNTVDELPGCLVAFSM----- 188
Qy      227 WSNNGRASCYVLESIGSHELTQ---DSRLQVINIDLKPGVQYNNIPYLOSNTKG 282
Db      189 WVGKNGINSSRETNNATTAHPNVRKPSGSDHGLHLPRL-GGPRMH-RPELDELRTSA 246
Qy      283 DPLGTEGLDASNTERSRAGSPAPVHDESLVGPVDPSSGQSRDTEVLVLGEPGTRYN 342
Db      247 LEMVAEQRLTQTPES-----PVD-----GLRGSILYT 275
Qy      343 ATVYSQANGTEGQPOAIEFTNALIOVEDVTAVANISATSLTLWKVSDNESSNYTKIH 402
Db      276 CSWVEKDGVSWSMRLVTSITTAHPNVRNLTVEAQNTSSIALTWVEPDGDPQNSTYGV 335
Qy      403 VAGETDSNINLVSPPRAVIRPLASSTPNTVYCVLADIBETPGLQVH----- 451
Db      336 YTGQGRA-----GTRSTAHNTITVDL-----EPCLLYFVSVWVKNGINS 377
Qy      452 -----TPVPVSDFRVTVVSTTEIGLAWSSDAE-----SFQMHITQAGNSRVEI 498
Db      378 SRETRNATTAPNVRNLTVEAQNTSSIALCBEVDGPRPDQYTYVWGTGGG-GGETERN 436
Qy      499 TTNSIIIGLFPSTKYCFEIVPXPNGTEGASRTVCNRYSAVFDIHVVYVTTKML 558
Db      437 TTNSVTAERLEPGLTITFSVMAE-KNGARSGQNVISITVPNAVTSLSKQDMNSTIAL 495
Qy      559 DWKSPD--GASEYYHL--VIESKGSNHSITDKAITLQGLIGTLNITISEVDHW 614
Db      496 RMTAPQGGQSSYSYVWWSVWEGMTDPRQTSQTDITLTKLEGLSLHLLVMAERNEVR 555
Qy      615 GDPNSTAQYRPSVNSINDVSTNTTAATLSQNF--DDASPTYGCLIEKAGN----- 666
Db      556 GYNSTLTRAIPANEVITDQNETQTKNSVMLWMAKAPGPHSGLIYVWQMASKGRPRQD 615
Qy      667 -SSNATQVNTDIGITDAVTELIPGSSYVVEIPAOVGDGKISLEPRKSPC--TDPASMA 723
Db      616 PQANWVQTSRNTNTWYKVEALEPGLTYNFTVMAERNDVASSTQ---SLCASTYPTVT 671
Qy      724 SPDCVVPKEPALVLYKTCPPGANAGFELEVSSGAMNATHLESCESSNGTEYREYVYL 783
Db      672 ITSCVSTISAGVNLIMSCPGGYEAPELEV-----GGCRGSDRS----- 712
Qy      784 NESTSVNISITTVSCGMMAPTNTCTGTTDPPPGSPNITSVSHSVKVSQFEAS 843
Db      713 -----SCGEAVS-----VLGL----- 723
Qy      844 HGPITKAYAVILTTGEAGHPASADVLKTYTDDPKKASDPTVYTYLIRTEBKRSQSLSEVLK 903
Db      724 -GPASYPATITT-----IMDGK-----VVS 744
Qy      904 YEIDVGNESITLYGNGKLEPLGSYRACVAGTNTTTHPQNGKILDGAEYSVSRISDA 963
Db      745 HSVVCHTESA----- 754
Qy      964 VSLPQDPGVICGAVGCIFGALVITVYGFIFMRKGRDAKNEVSPQIKPKSKL--- 1020
Db      755 -----GVLAGAVVGLI--LPLIVGLILFPLKRRKKK-----QQPELRDLVFS 797
Qy      1021 -----IRVENFEAFYKKQADNSCGFAEYEDLKLVGISQPKYAAELAEHRGKRRYNNVL 1076

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Db      798 SPGDIPADFPADHYRKNRSDNCGFADEYQOLSLVHGSQOMVYASASENNARKRYRNVLP 857
Oy      1077 YDISRYKLS-VQHTSTDDYINANMPGYSKQPIAIOGRLPNTLDPMFMWEEKVYVAI 1135
Db      858 YDMSRVLPKPIHEPBGSDYINASFMPGLMSPQEFIAIOGRLPQTVGDFRWLVWEQOQSHLT 917
Oy      1136 IMLTKEVQGRTKCEBYWP-SKQADYGDITVAMTSEIVLPEWTIRDFYKNIQTSSEHP 1194
Db      918 VMLTNCMEAGRVCCEHYWPLDSQPCETHGLRVTLVGESEWMENTVARELLILOVEBQKTLIS 977
Oy      1195 LROPHFTSWPDHGVDPDTLLINFRYLVRDYMKQSPESPILVHCSAGVGRGTFTAIIR 1254
Db      978 VROPHYQAMPDHGVPSPPDTLLAFWRMLRQMDQMEGGRPIVHCSAGVGRGTFTIADLV 1037
Oy      1255 LIYOIENENTVDYGYIYDLRMRPLMVQTEDOYVFLNOCVLDIYRSQ 1302
Db      1038 LLMQLOSEGLLGPFSFVRKMRRESRPLMVQTEAOYVFLHQCICGSSNSQ 1085

RESULT 14
US-10-245-539-8
; Sequence 8, Application US/10245539
; Publication No. US20030077638A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: MID 4460, A HUMAN TYROSINE PHOSPHATASE
; FILE REFERENCE: MP101-155PIRM
; CURRENT APPLICATION NUMBER: US/10/245,539
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: 60/323,018
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for windows Version 4.0
; LENGTH: 1118
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-245-539-8

Query Match      16.1%; Score 1130; DB 14; Length 1118;
Best Local Similarity 25.9%; Pred. No. 1.5e-60;
Matches 354; Conservative 181; Mismatches 453; Indels 380; Gaps 40;

Oy      8 AALLPERSPC-----LWALPILILILRLQOILCAGGTSPSPIDPSSVATVAT 53
Db      25 AALPAPNPGRLVTETQTSSISLSWEVP-----DGLDS--QNSNYVQCT 68
Oy      54 GENGITQISSTASFFHKQNGTGTPOVETNTSEDSGSGA--NDSLRTEQSGNGTDASQ 111
Db      69 GGGGTTERTNT-----TATNVYDGLGPGSLYTCSVWEKDGVSNGSVGT-- 112
Oy      112 KTPSSTGSPVFDIAKAVISPTNVLLTWKSNDDTAABRYK-YVVKHKMENEK--TITVVHQ 168
Db      113 -VTTATAPNPVNLHVEAQINSSIALTWEVDPGPDPQNSTGVEYTGCGAGRSTAH- 170
Oy      169 PWCNTT-GLRATSYVSIITPGIGNETWGPBRYKVTTEPIPVSDLRVALTVRKALIS 226
Db      171 --TNTVGLGEPGCLYAFSM-----PVD-----GGPGSLYLT 275
Oy      227 WSNNGTASCRVLLESIGSHELTQ---DSRLQVNIIDLKRGVQYININPYLLQSNKTKG 282
Db      189 WVGKNGINSRETRNATTAHNPRKRPESGSDHQLHLPCL-GGRRW-HRPELIDLRTSA 246
Oy      283 DPLGTGGLDASNTERSFAPSPTAFVHDESLVGPVDPSSGQSRDTEVLVGLPEGTRYN 342
Db      247 LEMVAEORLETOOTPEP-----PVD-----GGPGSLYLT 275
Oy      343 ALVYQAANGTEGQPOALEPRTNAIQVFDYTAVAISATSLTLWKVSDNESSNYTYKIH 402
Db      276 CSVWEKDGUNSSRWLVTSTTANPNRNLVTEAQINSSIALTWEVDPGPDPQNSTGYVE 335
Oy      403 VAGETDSSNLNVSEPRAVIPGLRSTFYNIIVCPVLADIGTPOGLVH----- 451

```

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Db      336 YTGDSGRA-----GTRSTAHNTNITVDRL-----EPCLYVFSVWGNKNGINS 377
Oy      452 -----TPVPVSDFRVTVVSTTEIGLAWSHDAE-----SPOMHTORAGANSREI 498
Db      378 SRETRNATTAHPNPVNLHMETQINSSIALCNEVDPGPRPODYIYWGVTGSG-GGTEFRN 436
Oy      499 TTNQSIITIGLFPFGTKYCFELVYPKPNGTGASRTVCNRPVAPFDIHVVYVTTTMMWL 558
Db      437 TYNSTVTAERLEPGLTYFYSVWAE-KNGARSGRQNVSIITVPNAVTSLSKQDWTNSTIAL 495
Oy      559 DKSPPD-GASEYVYHL--VIESKHGSHNSTYKATLTLQGLIGTLYNTITISEVHW 614
Db      436 RMTAPQGGQSSYSTWYSWWEKMTDPRTOSTSGTITLKELENGSLYHLITVMAERNEVR 555
Oy      615 GDNSTAOYTPRNVSNIDVSTNTTAATLSWQNF--DASPTYSCLLIEKAGN----- 666
Db      556 GYNSTLTAAATAPNEVTDLQNETQKNSSVMLMKAAPGDBHSQLYVYVQWASKGHPRRGD 615
Oy      667 -SSNATQVYVDIGITDATTVELIPGSSYVIEIFQVQVDGIKSLPEPKKSPC--TDPASMA 723
Db      616 PQAMVWVQTSRNTETWYKVEALEBGLTYNFTVMAERNDVASSTQ---SLCASTYPPDTVT 671
Oy      724 SPDECVVPKEBALVILKWTCPGANAGFELEYSAGMANNATHLSCESENGTEYRTETVYL 783
Db      672 ITSCVSTISAGVNLINSCPOGYEALELEY-----GGQRSGQDS----- 712
Oy      784 NFSTSVNISITWYSCGKMAAPRNTCTTGITDPPRDPGSENIITSVSHNVKVPFSGFEAS 843
Db      713 -----SCGAVS-----VLGL----- 723
Oy      844 HGP1KAYAVILITGEAHPADVLKTYDDPFKGAADTYTYTLIRTEBKRSQSLSEVYLK 903
Db      724 -GPARSYPATITTT-----IWDGK-----VVS 744
Oy      904 YEIDVGNESFTLLGYNGKLEPLGSYRACVAGFTNITFHPQNKGLIDGAEYSVFSRYSDA 963
Db      745 H5VVCHTESA----- 754
Oy      964 VSLPQDPGVICGAVFGICFALVIVYVGGFIEMRKRKKAQKANNVESPQIKPKKSLT--- 1020
Db      755 -----GVLAGAFVGLT---LFLILVGLLIFPLKRNKKK-----QOKELRDLVFS 797
Oy      1021 -----IRVENFEAYFKQOADSNGCFABEYEDLVLGVISOPKYAELAENRGNRYNVLP 1076
Db      798 SPGDIPADFPADHYRKNRSDNCGFADEYQOLSLVHGSQOMVYASASENNARKRYRNVLP 857
Oy      1077 YDISRYKLS-VQHTSTDDYINANMPGYSKQPIAIOGRLPNTLDPMFMWEEKVYVAI 1135
Db      858 YDMSRVLPKPIHEPBGSDYINASFMPGLMSPQEFIAIOGRLPQTVGDFRWLVWEQOQSHLT 917
Oy      1136 IMLTKEVQGRTKCEBYWP-SKQADYGDITVAMTSEIVLPEWTIRDFYKNIQTSSEHP 1194
Db      918 VMLTNCMEAGRVCCEHYWPLDSQPCETHGLRVTLVGESEWMENTVARELLILOVEBQKTLIS 977
Oy      1195 LROPHFTSWPDHGVDPDTLLINFRYLVRDYMKQSPESPILVHCSAGVGRGTFTAIIR 1254
Db      978 VROPHYQAMPDHGVPSPPDTLLAFWRMLRQMDQMEGGRPIVHCSAGVGRGTFTIADLV 1037
Oy      1255 LIYOIENENTVDYGYIYDLRMRPLMVQTEDOYVFLNOCVLDIYRSQ 1302
Db      1038 LLMQLOSEGLLGPFSFVRKMRRESRPLMVQTEAOYVFLHQCICGSSNSQ 1085

RESULT 15
US-10-245-539-4
; Sequence 4, Application US/10245539
; Publication No. US20030077638A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; TITLE OF INVENTION: MID 4460, A HUMAN TYROSINE PHOSPHATASE
; FILE REFERENCE: MP101-155PIRM

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CURRENT APPLICATION NUMBER: US/10/245,539
CURRENT FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: 60/323,018
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1093
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: consensus sequence
US-10-245-539-4

Query Match 16.0%; Score 1127; DB 14; Length 1093;
Beet Local Similarity 26.3%; Pred. No. 2,2e-60;
Matches 344; Conservative 177; Mismatches 438; Indels 350; Gaps 37;

53 TGENGITOISSTAESFHKQNGTGTQVETNTSEDESSGA--NDSLRTPGQSNGTGAS 110
43 TGDGTTETRT-----TATNTYVDLGSGSLYTCGVWVWKKGVASVGT- 87
QY 111 QKTPSTGSPVFDIKAVISPTNVLTKSNDTASEYK-YVVKHKNENEK--TITVH 167
Db 88 --VTTATAPNPNRNLRAQNTSSIALTWEVDPDPQNSTGYVEYTGDCGAGTRSTAH 145
QY 168 QPKCNIT--GIRPATSYFSTITPGIGNETWGDPRVIXITEPIVSDLRVALTGRKAL 225
Db 146 ---TNTYVDLGSGSLYAFSM----- 163
QY 226 SMSNGTASGCRVLLSISGHELTQ---DSRLQVNSDLKPGVQYINPYLQSNKTK 281
Db 164 -WVGKNGINSRRETRNATTAAHPVAKPKPSSGSDHQLHPEL-GGFRMH-RPELDLRLTS 220
QY 282 GDPLEGTGCLDASNTERSRAGSPTRPVHDESLVGPVDPSSGQSHRTEVLLVLEPGTRY 341
Db 221 ALEWVAEQRLETCQTPES-----FVD-----GLGPGSLY 249
QY 342 NATYYSQAANGTEGQPOAIEPTNAIQVDTAVANISATSLTLTKVSDNESSNYTKI 401
Db 250 TCSVWVEKDVNSSSWRLVSTTAPNPNRLTVEAQNTSSIALTWEVDPDPQNSTGYV 309
QY 402 HVAGETDSNLNVSEPRAVIPGLRSTFYNTVCPVLGDIETPGFLQVH----- 451
Db 310 EYTGDGNA-----GTRSTANTNITVDRL-----EPGCLYFVSVMVKGKGIN 351
QY 452 -----TPPVVSDPRVTVVSTTEIGLAWSSHAD-----SFQMHITGEGANSRVE 497
Db 352 SSRERNTATTAHPNPNRLHMETQNTSSIALCWEVPDGPYPQDYTWVGVTGDC--GGTEFR 410
QY 498 ITTNOSIIIGLFPCTKCFEIVPKGPNGTGASRTVCNRTYPSAVFDIHVVYVTTTBMW 557
Db 411 NTNTSVTAERLEPGLTLYFSVMAE-KNGARGSRQNVISITVPAVTSLSKQDWTNSTIA 469
QY 558 LDKWSPD--GASEVYVYH--VLESKGSNHTSYDKAITLOGLIPGLYNITISPEVDHV 613
Db 470 LKMTAPGCPGQSSSYWVSWVREGMTDPRTOSTGTDITLKELEKSLIHLTWAEERNEV 529
QY 614 WGDPNSTAQYTRPSNVSNIDVSTNTTAATLSWQNF--DDASPTYSCULLIERAGN----- 666
Db 530 RGYNSTLTAATAPNNEVTDLOMETQTKNSVLMWKARPDHSQLYVWVQWASKGHPRGQ 589
QY 667 --SSNATOVVTDIGITDAVTTELIIGSSYVEIFPAQVGDGKISLEPRGKSF--TDPASM 722
Db 590 DPOANWVWQTSRNETWYKVEALEPGLTYNFTVMAERNDVASSTQ---SLCASYPDTV 645
QY 723 ASPDEVVPKPRALVLYKWTCPGANAGFELEVSSGAMNNAATLBSCSSENGTEVTEVY 782
Db 646 TITSCVSTISAGYVNLWSCPGQGEARELEV-----GGQKRSQDRS----- 687
QY 783 LNFSTSYNISITTVSCGMAAFTRTCTGTIDPPPPGSPNITSVSHNSVVKFSGFEA 842
Db 688 -----SCGEAVS-----VLGL----- 698

QY 843 SHGPIKAYAVLLTTEAGHPESADVLKTYDDPFKKGASDTVYTLIRTEEKRQSQSLSEVL 902
Db 699 --GPASTPATIT-----IMDMK-----VV 718
QY 903 KYEIDVGNESSTLIGYNGKLEPLGASYRACVAGFTNITFHPQNKGLDGAESYVSFSRYSD 962
Db 719 SHSVYCHTESA----- 729
QY 963 AVSLPQDBGVICGAVPGCIFGALVIVTVGGRIFPKRKRKAKKNNVSRSQIKPKSKYL-- 1020
Db 730 -----GVYAGAFVIGIL--LFLILVGLLIFLKRNNKK-----QOKPELRDLVF 771
QY 1021 -----IRVENPEAFKKQADNSGCFABEYEDLKLVGISOPKYAAELAEENRGRYNNVL 1075
Db 772 SSPBDIPAEADYKRNKRNSCGFPADEYQSLVGHSSQGMVYASASENNAKRRYRNVL 831
QY 1076 PYDISRYVLS-VQTHSTDDYINANYMPGYSKKQFIATQGPLPNTLKDPMWVWEKUNYA 1134
Db 832 PYDMSRVPLKPIHEPSPSDYINASFMPGLMSPQEFIAIQGPLPQTVGDFWRLVWEQSH 891
QY 1135 IIMITKCYEGORTCEERYWPK-SKQADYGDITVAMTSEIVLPWTIRDFYKNIQTSSEH 1193
Db 892 LVMELTNCMEAGRVCCEHYWPLDSQCTGHGLRVTLVGEVEWENWTVRELILLQVEEQKTL 951
QY 1194 PLRQFHTSWPDHGVPTDILLINFRYLVRDYMKSQSPESPILVHCSAGVGTGTFIAD 1253
Db 952 SVRQFHTQAMPDGHVPSPTLLAFMRMLRQMLQTMGEGFPYHCSAGVGTGTLIAD 1011
QY 1254 RLIVQIENENTVDYGIYVDLRMRPLMVQOTEDQVFLNQCVLDIVSQ 1302
Db 1012 VLLNQLOSEGLGPFSPYRKKRESRPLMVQTEAGYVFLHQICICSSNSQ 1060

Search completed: May 10, 2005, 19:09:31
Job time : 189 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:54:46 ; Search time 53 Seconds
(without alignments)
2427.204 Million cell updates/sec

Title: US-09-516-728A-4
Perfect score: 7030
Sequence: 1 MKPARARARLPFRSPGLRWA.....TIVENLAPVTTFKINGYIA 1337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6826	97.1	1337	1	protein-tyrosine-p
2	4508.5	64.1	1238	2	HRP beta-like tyr
3	1242	17.7	1997	1	protein-tyrosine-p
4	1130	16.1	1118	1	protein-tyrosine-p
5	1028	14.6	1630	2	protein-tyrosine-p
6	1026	14.6	1557	2	protein-tyrosine-p
7	981.5	14.0	583	2	protein-tyrosine-p
8	957.5	13.6	1711	1	protein-tyrosine-p
9	954	13.6	1767	2	protein-tyrosine-p
10	949	13.5	1615	2	protein-tyrosine-p
11	879	12.5	1912	2	protein-tyrosine-p
12	864	12.3	2302	2	protein-tyrosine-p
13	854	12.1	1188	1	protein-tyrosine-p
14	842	12.0	1187	1	protein-tyrosine-p
15	839	11.9	1216	2	protein-tyrosine-p
16	834.5	11.9	1622	2	protein-tyrosine-p
17	832	11.8	1691	1	protein-tyrosine-p
18	829	11.8	1894	2	protein-tyrosine-p
19	817	11.6	1367	2	protein-tyrosine-p
20	807	11.5	1898	2	protein-tyrosine-p
21	795.5	11.3	1863	1	protein-tyrosine-p
22	792.5	11.3	1897	1	protein-tyrosine-p
23	787.5	11.2	1907	2	protein-tyrosine-p
24	785.5	11.2	1452	1	protein-tyrosine-p
25	771.5	11.0	1452	1	protein-tyrosine-p
26	767	10.9	1437	2	protein-tyrosine-p
27	764	10.9	1290	2	protein-tyrosine-p
28	761	10.8	2051	2	protein-tyrosine-p
29	750	10.7	2029	1	protein-tyrosine-p

30	742	10.6	1499	2	protein-tyrosine-p
31	739.5	10.5	1501	2	protein-tyrosine-p
32	728.5	10.4	1262	1	protein-tyrosine-p
33	728.5	10.4	1496	1	protein-tyrosine-p
34	722.5	10.3	405	2	protein-tyrosine-p
35	722.5	10.3	405	2	protein-tyrosine-p
36	704	10.0	2314	1	protein-tyrosine-p
37	693	9.9	1585	2	protein-tyrosine-p
38	688.5	9.8	1440	2	protein-tyrosine-p
39	678.5	9.7	1457	1	protein-tyrosine-p
40	674.5	9.6	1301	1	protein-tyrosine-p
41	669	9.5	1445	1	protein-tyrosine-p
42	664	9.4	1442	1	protein-tyrosine-p
43	656.5	9.3	1422	2	protein-tyrosine-p
44	640.5	9.1	1435	2	protein-tyrosine-p
45	636.5	9.1	1304	1	protein-tyrosine-p

ALIGNMENTS

RESULT 1
138670 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human
N:Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase
C:Species: Homo sapiens (man)
C>Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 09-Jul-2004
C:Accession: 138670, 152599
R:Ostman, A.; Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
A>Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced
A:Reference number: 138670, PMID:95024024, PMID:7937872
A:Accession: 138670
A:Molecule type: mRNA
A:Residues: 1-1337 <RES>
A:Cross-references: UNIPROT:Q12913; EMBL:U10886; NID:9558754; PID:9558755
A:Experimental source: HeLa cells
R:Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.
Blood 84, 4186-4194, 1994
A>Title: Molecular cloning, characterization, and chromosomal localization of a novel pr
A:Reference number: 152599, PMID:95086212; PMID:7994032
A:Accession: 152599
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-216, 'LNGVRRKA', 225-260, 'G', 262-285, 'GTEGGDASNTERRSA', 302, 'S', 304, 'TAPVHDE
A:Cross-references: GB:D37781; NID:9633072; PID:BA07035.1; PID:9633073
C:Comment: Enhanced expression of this protein with increasing cell density suggests a r
C:Genetics:
A:Gene: GDB:PTPRJ
A:Cross-references: GDB:1385040; OMIM:600925
A:Map position: 19q13.4-19q13.4
C:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and
A:Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repea
C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; receptor; tran
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1337/Product: protein-tyrosine-phosphatase, receptor type J #status predicted <MAT>
F:118-197/Domain: fibronectin type III repeat homology <3FNB>
F:206-283/Domain: fibronectin type III repeat homology <3FNB>
F:284-356/Domain: fibronectin type III repeat homology #status atypical <3FNC>
F:365-445/Domain: fibronectin type III repeat homology <3FNB>
F:453-530/Domain: fibronectin type III repeat homology <3FNB>
F:539-617/Domain: fibronectin type III repeat homology <3FNB>
F:720-804/Domain: fibronectin type III repeat homology <3FNB>
F:972-988/Domain: transmembrane #status predicted <TMN>
F:1065-1287/Domain: protein-tyrosine-phosphatase homology <PYP>
F:172-82, 93, 104, 142, 172, 192, 231, 258, 276, 342, 351, 376, 391, 396, 413, 501, 525, 536, 582, 603, 6
F:1239/active site: Cys (phosphotyrosine intermediate) #status predicted
F:1245/Binding site: substrate phosphate (Arg) #status predicted

Query Match 97.1%, Score 6826, DB 1, Length 1337,
Best Local Similarity 97.5%, Pred. No. 0,
Matches 1303, Conservative 5, Mismatches 29, Indels 0, Gaps 0;

```

QY      1 MKPAAREARLPSPSPGLRMLPLLLLLRLGOLLGAGTSPSPIDPSVAIVATGNGINTQ 60
      1 MKPAAREARLPSPSPGLRMLPLLLLLRLGOLLGAGTSPSPIDPSVAIVATGNGINTQ 60
Db      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEBOGNGTGDASQKTPSSGTGS 120
QY      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEBOGNGTGDASQKTPSSGTGS 120
Db      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEBOGNGTGDASQKTPSSGTGS 120
QY      121 PVVDIAVASISPTNNVLLTWKSNNTASSEKYVVKHMEKNTTVVHQWCNITGLRPAIT 180
      121 PVVDIAVASISPTNNVLLTWKSNNTASSEKYVVKHMEKNTTVVHQWCNITGLRPAIT 180
Db      121 PVVDIAVASISPTNNVLLTWKSNNTASSEKYVVKHMEKNTTVVHQWCNITGLRPAIT 180
QY      181 SYVFSITPGIGNETWGDPRVIVKITEPIVPSDLRVALTGVRAKALSMNGNGTASCRVLL 240
      181 SYVFSITPGIGNETWGDPRVIVKITEPIVPSDLRVALTGVRAKALSMNGNGTASCRVLL 240
Db      181 SYVFSITPGIGNETWGDPRVIVKITEPIVPSDLRVALTGVRAKALSMNGNGTASCRVLL 240
QY      241 ESIGSHEELTODSRLOVNIISDLKPGVQVINPYLLQSNKTKGDPLEGGLDASNTERSR 300
      241 ESIGSHEELTODSRLOVNIISDLKPGVQVINPYLLQSNKTKGDPLEGGLDASNTERSR 300
Db      241 ESIGSHEELTODSRLOVNIISDLKPGVQVINPYLLQSNKTKGDPLEGGLDASNTERSR 300
QY      301 AGSPPTAPVHDESLVGPVDPSSGQOSRDTEVLLVGLBPRGRNATYYSQANGTGQOPAI 360
      301 AGSPPTAPVHDESLVGPVDPSSGQOSRDTEVLLVGLBPRGRNATYYSQANGTGQOPAI 360
Db      301 AGSPPTAPVHDESLVGPVDPSSGQOSRDTEVLLVGLBPRGRNATYYSQANGTGQOPAI 360
QY      361 EFRINAIOVEDYAVANISATSLTLTWKVSNDNESSNYTKIHVAGETDSNLTNGEPRAY 420
      361 EFRINAIOVEDYAVANISATSLTLTWKVSNDNESSNYTKIHVAGETDSNLTNGEPRAY 420
Db      361 EFRINAIOVEDYAVANISATSLTLTWKVSNDNESSNYTKIHVAGETDSNLTNGEPRAY 420
QY      421 IGLRSTSTYNTTCVGLDICTGPGFLQVHPVPVSDPRVTVSTTEIGLWAMSHDAE 480
      421 IGLRSTSTYNTTCVGLDICTGPGFLQVHPVPVSDPRVTVSTTEIGLWAMSHDAE 480
Db      421 IGLRSTSTYNTTCVGLDICTGPGFLQVHPVPVSDPRVTVSTTEIGLWAMSHDAE 480
QY      481 SFQOMHITOGAGNSRVEITTTNOSIIIGLFGPKTKCFELVPGKPGTGSASTVCNRTVP 540
      481 SFQOMHITOGAGNSRVEITTTNOSIIIGLFGPKTKCFELVPGKPGTGSASTVCNRTVP 540
Db      481 SFQOMHITOGAGNSRVEITTTNOSIIIGLFGPKTKCFELVPGKPGTGSASTVCNRTVP 540
QY      541 SAVFDIHVVYVTTTMMWMDMKSPPDGASEVYVHLVIESKHSNHTSTYDKAILTQGLIPGT 600
      541 SAVFDIHVVYVTTTMMWMDMKSPPDGASEVYVHLVIESKHSNHTSTYDKAILTQGLIPGT 600
Db      541 SAVFDIHVVYVTTTMMWMDMKSPPDGASEVYVHLVIESKHSNHTSTYDKAILTQGLIPGT 600
QY      601 LYNITISPEVDHVMGDDPNSTAQYTPRSNVSNIDVTNTTAATLSMQNDDASPTYSYCLL 660
      601 LYNITISPEVDHVMGDDPNSTAQYTPRSNVSNIDVTNTTAATLSMQNDDASPTYSYCLL 660
Db      601 LYNITISPEVDHVMGDDPNSTAQYTPRSNVSNIDVTNTTAATLSMQNDDASPTYSYCLL 660
QY      661 IEKANSSNATQVVTDIGITDATTVELIPGSSYVTEIFAQVGDGKSLBPRKSFCTDPA 720
      661 IEKANSSNATQVVTDIGITDATTVELIPGSSYVTEIFAQVGDGKSLBPRKSFCTDPA 720
Db      661 IEKANSSNATQVVTDIGITDATTVELIPGSSYVTEIFAQVGDGKSLBPRKSFCTDPA 720
QY      721 SMASTDCVVPKEPALVLTCTCPGANAAGFELVSSGAMNNATHLESSENGTEYRTREV 780
      721 SMASTDCVVPKEPALVLTCTCPGANAAGFELVSSGAMNNATHLESSENGTEYRTREV 780
Db      721 SMASTDCVVPKEPALVLTCTCPGANAAGFELVSSGAMNNATHLESSENGTEYRTREV 780
QY      781 TYLANSTSTNISITTVSCGMAAPTRNTCTGTTDPPPDGSPNTTSVSHSVYKSGE 840
      781 TYLANSTSTNISITTVSCGMAAPTRNTCTGTTDPPPDGSPNTTSVSHSVYKSGE 840
Db      781 TYLANSTSTNISITTVSCGMAAPTRNTCTGTTDPPPDGSPNTTSVSHSVYKSGE 840
QY      841 EASHGPIKAYAVIILTTGAGHPSADVLTCTYDDFKKASDITYVYLIRTEBKGRSOSLSE 900
      841 EASHGPIKAYAVIILTTGAGHPSADVLTCTYDDFKKASDITYVYLIRTEBKGRSOSLSE 900
Db      841 EASHGPIKAYAVIILTTGAGHPSADVLTCTYDDFKKASDITYVYLIRTEBKGRSOSLSE 900
QY      901 VLKXIDIVGNESSTLGYNGKLEPFGSRYACVAGTNTTFHPONKGLIDGASVYSFSRY 960
      901 VLKXIDIVGNESSTLGYNGKLEPFGSRYACVAGTNTTFHPONKGLIDGASVYSFSRY 960
Db      901 VLKXIDIVGNESSTLGYNGKLEPFGSRYACVAGTNTTFHPONKGLIDGASVYSFSRY 960
QY      961 SDAVSLPODPGVICGAVFGCIFGALVITYGSGFIMRKGRKADANNEVSFOIIPKXSKL 1020
      961 SDAVSLPODPGVICGAVFGCIFGALVITYGSGFIMRKGRKADANNEVSFOIIPKXSKL 1020
Db      961 SDAVSLPODPGVICGAVFGCIFGALVITYGSGFIMRKGRKADANNEVSFOIIPKXSKL 1020
QY      1021 IRVENFEAFYFKQOADSNGFAEEYEDLKLVGISQPKYAAELANRGNRYNNVLPYDIS 1080
      1021 IRVENFEAFYFKQOADSNGFAEEYEDLKLVGISQPKYAAELANRGNRYNNVLPYDIS 1080
Db      1021 IRVENFEAFYFKQOADSNGFAEEYEDLKLVGISQPKYAAELANRGNRYNNVLPYDIS 1080

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QY      1081 RYKLSVQTHSDPDYINANMYGHSKDPFIATOGPLPNTLKDQFMRMWEKXVYAIIMLTK 1140
      1081 RYKLSVQTHSDPDYINANMYGHSKDPFIATOGPLPNTLKDQFMRMWEKXVYAIIMLTK 1140
Db      1081 RYKLSVQTHSDPDYINANMYGHSKDPFIATOGPLPNTLKDQFMRMWEKXVYAIIMLTK 1140
QY      1141 CVEQGRTCCEYWSKQADGDIIVAMTSEIIVPEMTIRDFYKNIQTSSEHPLRQPHF 1200
      1141 CVEQGRTCCEYWSKQADGDIIVAMTSEIIVPEMTIRDFYKNIQTSSEHPLRQPHF 1200
Db      1141 CVEQGRTCCEYWSKQADGDIIVAMTSEIIVPEMTIRDFYKNIQTSSEHPLRQPHF 1200
QY      1201 TSPDPHGVPTDITLLINFRYVDRYMKQSPESPILVHCSAGVGTGFIAIDRLIYQIE 1260
      1201 TSPDPHGVPTDITLLINFRYVDRYMKQSPESPILVHCSAGVGTGFIAIDRLIYQIE 1260
Db      1201 TSPDPHGVPTDITLLINFRYVDRYMKQSPESPILVHCSAGVGTGFIAIDRLIYQIE 1260
QY      1261 NENTVDVGIYDILRMHRLPMAVOTEDQVFLNQCULIVSQRXKVDLIYONTANTIIY 1320
      1261 NENTVDVGIYDILRMHRLPMAVOTEDQVFLNQCULIVSQRXKVDLIYONTANTIIY 1320
Db      1261 NENTVDVGIYDILRMHRLPMAVOTEDQVFLNQCULIVSQRXKVDLIYONTANTIIY 1320
QY      1321 ENLAPVTTFGKTXGYIA 1337
      1321 ENLAPVTTFGKTXGYIA 1337
Db      1321 ENLAPVTTFGKTXGYIA 1337

```

RESULT 2

```

S68700
HPTP beta-1-like tyrosine phosphatase precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C.Accession: S68700
R.Kunimochi, S.; Matsuoka, S.; Saitoh, T.; Ohnogi, M.; Yamamoto, T.
FEBS Lett. 378, 7-14, 1996
A.Title: Molecular cloning and characterization of Byd, a murine receptor-type tyrosine k
A.Reference number: S68700; MUID:96140699; PMID:8549806
A.Accession: S68700
A.Status: Preliminary; nucleic acid sequence not shown
A.Molecule type: mRNA
A.Residues: 1-1238 <ROR>
A.Cross-references: UNIPROT:Q64455; GB:D45212; NID:g1208432; PIDN:BA08146.1; PID:g120843
C.Genetics:
A.Map position: 281-2
C.Superfamily: protein-tyrosine-phosphatase, receptor type U; fibronectin type III repeat
C.Keywords: phosphoprotein
P.1-28/Domain: signal sequence #status predicted <SIG>
P.29-1238/Product: HPTP beta-1-like tyrosine phosphatase #status predicted <MAT>
P.267-347/Domain: fibronectin type III repeat homology <3PR>
P.966-1188/Domain: protein-tyrosine-phosphatase homology <PPP>
P.1140/Active site: Cys (phosphocysteine intermediate) #status predicted
P.1146/Binding site: substrate phosphate (Arg) #status predicted

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Query Match      64.1%; Score 4508.5; DB 2; Length 1238;
Best Local Similarity 67.2%; Pred. No. 1.5e-244;
Matches 901; Conservative 108; Mismatches 226; Indels 105; Gaps 12;

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QY      1 MKPAAREARLPSPSPGLRMLPLLLLLRLGOLLGAGTSPSPIDPSVAIVATGNGINTQ 60
      1 MKPAAREARLPSPSPGLRMLPLLLLLRLGOLLGAGTSPSPIDPSVAIVATGNGINTQ 60
Db      1 MKPAAREARLPSPSPGLRMLPLLLLLRLGOLLGAGTSPSPIDPSVAIVATGNGINTQ 60
QY      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEBOGNGTGDASQKTPSSGTGS 120
      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEBOGNGTGDASQKTPSSGTGS 120
Db      61 ISSSTAFPHKONGTGPQVETNTSEDESSGANDSLRTEBOGNGTGDASQKTPSSGTGS 120
QY      121 PVVDIAVASISPTNNVLLTWKSNNTASSEKYVVKHMEKNTTVVHQWCNITGLRPAIT 180
      121 PVVDIAVASISPTNNVLLTWKSNNTASSEKYVVKHMEKNTTVVHQWCNITGLRPAIT 180
Db      121 PVVDIAVASISPTNNVLLTWKSNNTASSEKYVVKHMEKNTTVVHQWCNITGLRPAIT 180
QY      181 SYVFSITPGIGNETWGDPRVIVKITEPIVPSDLRVALTGVRAKALSMNGNGTASCRVLL 240
      181 SYVFSITPGIGNETWGDPRVIVKITEPIVPSDLRVALTGVRAKALSMNGNGTASCRVLL 240
Db      181 SYVFSITPGIGNETWGDPRVIVKITEPIVPSDLRVALTGVRAKALSMNGNGTASCRVLL 240
QY      241 ESIGSHEELTODSRLOVNIISDLKPGVQVINPYLLQSNKTKGDPLEGGLDASNTERSR 300
      241 ESIGSHEELTODSRLOVNIISDLKPGVQVINPYLLQSNKTKGDPLEGGLDASNTERSR 300
Db      241 ESIGSHEELTODSRLOVNIISDLKPGVQVINPYLLQSNKTKGDPLEGGLDASNTERSR 300
QY      301 AGSPPTAPVHDESLVGPVDPSSGQOSRDTEVLLVGLBPRGRNATYYSQANGTGQOPAI 360
      301 AGSPPTAPVHDESLVGPVDPSSGQOSRDTEVLLVGLBPRGRNATYYSQANGTGQOPAI 360
Db      301 AGSPPTAPVHDESLVGPVDPSSGQOSRDTEVLLVGLBPRGRNATYYSQANGTGQOPAI 360

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Db 204 PV-TNLSQAHKNSLVS-VDPSGQDPSLTLEILLTDKEDPTQYNAIIVSQAANGTEGQPRN 261
Qy 360 IEEPTNAIOVEDYNAVNISATSLTIKWYSDNESSNTYKIHVAGFDSNLANVSEBRA 419
Db 262 KVFKNSTQVSDVRKMNISASMTLTKMSNDGSTSTSVYKIHVAGGHSVNGVQNKKEA 321
Qy 420 VIPGLRSSTFNIVTCPLVIGDIETGPGFLQVHTPPVPVSDPRVTVASTTEIGLAWSSDA 479
Db 322 IILGLSSSTLVNITHPFLGQEGTGFGLQVYTSDDQSDPRVTVSTRALGLAMRSNDS 381
Qy 480 ESPQMHITOEGAGNSRVEITTNQSIIGLPEPTKYCEIIVPKGNGTEGASRTVCNRTV 539
Db 382 KSFEIPIKQDGEKERNASTGQSYVEDLKGTSYHEIILIPRGDGTGEGSLTNGSTD 441
Qy 540 PSAVFDIHVVYVTTTEMLDMKSPGASEVYVHVIVIEKHS-NTSTYDAITLQGLIP 598
Db 442 PSAVTDIRVNIITTEMLDMQNTDASGYVHVLKESKSGSIRFNSSQKMTVGLSLP 501
Qy 599 GTLVNITISPEVDHWGDPNSTAQYTRPSNVSNIDVNTTAAATLSMQNFDASPTVSYC 658
Db 502 GTLVNITIFPEVDQIGISNSTQYTRPSVSHIEVNTTTTAAIRMKNEBDAASVAYS 561
Qy 659 LLIEXAGNSSNAQVYT-DIGITDVTTELLIPSSYVEIFAQVGDGKSLPEPKSFT 717
Db 562 VLIKTKGDSNVTSNFTQDPSI---LIPELIPGVSYVAKILITQVGDGTTSLVPGWNLFC 618
Qy 718 DPASASDCEVVPREPALVLTCTCPRGANGFELEVSAGMNNATHLESCSENGCTYR 777
Db 619 EPEPTSTHCEVVPREPALVLTMACPFMYTGFELEVSADSMNTRLENCSTDDTDCR 678
Qy 778 TEVTYLNSTSYNISITTVSCGKMAAPTRNTCTTITPPPPDGSPNTSVSHNVKXKF 837
Db 679 TEVAYLNSTSYNISIALTSCGKALPAONICTTITPPPPDGSPNTSVSHNVKXKF 738
Qy 838 SGFEASHQPIKAYAVIILTTGEAHSADVLTCTYDFFKASDIYVYLLIITEKGSQS 897
Db 739 SGFEASHQPIKAYAVIILTTGEAHSADVLTCTYDFFKASDIYVYLLIITEKGSQS 798
Qy 898 LSEVLAKYEDVNGESTTIGYNGKLEPIGSTRACVAGTNTTFHQNGKLDGASYSYF 957
Db 799 LSEVLAKYEDVNGESTTIGYNGKLEPIGSTRACVAGTNTTFHQNGKLDGASYSYF 858
Qy 958 SRYSDAVSLPODPGICGAVFGCIGALVIYTVGFIEMRKRRKAKANNVFSQIKPK 1017
Db 859 SPYSEAVLFPDPPGICGAVFGCIGALAITRAGFIFMRKKRTAKANNVFSQIKPK 918
Qy 1018 SKLIRVENFEAYFKKQADSNCGFAEYEDLKLIGISLPKTAETAEENRGRKRYNNVLPY 1077
Db 919 SKLIRVENFEAYFKKQADSNCGFAEYEDLKLIGISLPKTAETAEENRGRKRYNNVLPY 978
Qy 1078 DISRVKLSVQTHSTDDYINANMPGYHSGKOPFATQGPLPNTLKPFRMVMWEXNYVALIM 1137
Db 979 DISRVKLSVQTHSTDDYINANMPGYHSGKOPFATQGPLPNTLKPFRMVMWEXNYVALIM 1038
Qy 1138 LTKCVOGRTKCEEWPSKQADYDITVAMTSEIVLPEWTRIDPTVKNIQTSSEHPLRQ 1197
Db 1039 LTKCVOGRTKCEEWPSKQADYDITVAMTSEIVLPEWTRIDPTVKNIQTSSEHPLRQ 1098
Qy 1198 FHTSPMDHGVDDTDLINFRYLVRYDMKQSPSPSPILVHCSAGVGTGTFIADRLIY 1257
Db 1099 FHTSPMDHGVDDTDLINFRYLVRYDMKQSPSPSPILVHCSAGVGTGTFIADRLIY 1158
Qy 1258 QIENENTVDYGIYVDLDMHRPLMQTEDQYVFLNQCLDIYRSQKSKDLIYQNTTAM 1317
Db 1159 QIENENTVDYGIYVDLDMHRPLMQTEDQYVFLNQCLDIYRSQKSKDLIYQNTTAM 1218
Qy 1318 TIYENLAPVTTEGKTNGYIA 1337
Db 1219 TIYENLAPVTTEGKTNGYIA 1238

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RESULT 3
S12050

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protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S12050; S15818; S15819
R:Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A>Title: Structural diversity and evolution of human receptor-1like protein tyrosine phos
A:Reference number: S12049; MUID:91006018; PMID:2170109
A:Accession: S12050
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1997 <KXU>
A:Cross-references: UNIPROT:P23467; GB:X54131; NID:935787; PIDN:CAA38066.1; PID:935788
R:de Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.
FEBS Lett. 282, 285-288, 1991
A>Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.
A:Reference number: S15818; MUID:91243813; PMID:1645282
A:Accession: S15818
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1911, 'VAMVLOK' <VRI>
A:Accession: S15819
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1872-1997 <VR2>
C:Genetic:
A:Gene: GDB:PTPRB; PTPB
A:Cross-references: GDB:127352; OMTM:176882
A:Map position: 12q15-12q21
C:Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-1997/Product: protein-tyrosine-phosphatase, receptor type beta #status predicted <W
F:23-1625/Domain: extracellular #status predicted <EXT>
F:1626-1642/Domain: transmembrane #status predicted <TM>
F:1643-1997/Domain: intracellular #status predicted <INT>
F:1727-1952/Domain: protein-tyrosine-phosphatase homology <PR>
F:1904/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1910/Binding site: substrate phosphate (Arg) #status predicted

Query Match 17.7%; Score 1242; DB 1; Length 1997;
Best Local Similarity 29.6%; Pred. No. 4.1e-61;
Matches 397; Conservative 190; Mismatches 503; Indels 251; Gaps 53;

Qy 123 FDIKAVGISPTNVLTWMSNTAASRYVVKHMKNEKTTTVHQPKWNTGLRPAATSY 182
Db 759 FDHYEVITKKNKNTFIQTSP-----KSENE-----CVFVQLVGRLY 796
Qy 183 VFSITPGIG---NETMGDPVIVIKTEPIVPSDLRVALTGVRKAALSMNGNGTASGRV 238
Db 797 SVYITTKSGQYEAHQ-GNGRTI-----PEVVDULTLRNRTEDLHVTVSGANG----- 844
Qy 239 LLESIGSH-ELTQDSRL-----OVNISDLKPVQY-----NINPYLLQSKNT 280
Db 845 ---DVDQYEQILFNDMKVFPFPHLVNTATYRFTSLTPGRQYKILVLTIGDVQOQSAFI 901
Qy 281 KG-----DPLG-----TEGLDLSN-----TERRSGRSPAPRHDSL 313
Db 902 EGFVPSAVKNIHISPNKATDSLTVNMTPGGGDVDSYTVSAPRRSQKDSQTIPIGH---- 957
Qy 314 VGPVDPSSGQGSRTLEVLLVGLPEGTRYNATVYVQAANGTEGQPOAIEFTNAIOVDPVT 373
Db 958 -----VFHTFHLLEAGEQQIMIAS--VSGSLKNGQINVGKRVTPASVQSVI 1002
Qy 374 AVN-ISAATSLTLIKVSDNESSSVYTKIHVAGETSSNLNVSEBRA-----VIPGL 424
Db 1003 ADNAVSSYSLIVSQAKAGVAE---RYDILLTLTENGILLRNTSEBATTQKHFFEDLTPGK 1059
Qy 425 RSTFTYNTVCVPGDIEGTGFLQVHTPPVPVSDPRVTVASTTEIGLAWSSDAESQW 484
Db 1060 K---YKIQILLTVSGGFSKEAQTEGRVPAVVDLRTENSTHRLSRMTASBGLSWY 1115
Qy 485 HI---TQEGAGNSRVEI-TTNQSIIGGLPFGTKYCEIIVPKGNGTEGASRTVCNRTVP 540

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Db      1116 NIFLYNPDGNLQERAGVDPLVQSFSPONLQGRMYMVLYTH--SGELSNESIFERTY 1173
Qy      541 SAFFDHHVYVTTT-MWLDKSPDQASEVYVHLVESHKGSNHSITTKAIT--LQGL 596
Db      1174 ASVSHLRGSRNNTTDSLWFNWSPASDQDFE-YELIYNNGTKCKENWKCKDKIDWFRFOGL 1232
Qy      597 IPEGLYNTITSPEDVHVGDPNSTAQYTR-----PANVSNIDVSTNTATL-----SWON 647
Db      1233 VPERKTVLVW---VTHSGDLNKNVTHESKRASPEPLMEFADIANSLAITKGPDPWD 1289
Qy      648 FDIASPTV---SYCLIEKAGNSNAQTQVYTDIGTDAITVTEIIPGSSVTEIFAQVGDG 704
Db      1290 YNDFELQWLPRLALTVFNPNYNNKSKRGRIYVG-----LRPGRSYQFNVKTVSGDS 1339
Qy      705 IKSL-EPGRKSFCTDASMASFDCVVPKBPALVLMKTCPPQANMGELEVSAGMNNAT 763
Db      1340 WKTYSPFISGVATTKDKIQNLHCR-PQNSTAIACSWIPDDSDPDGYSIE-----CR 1390
Qy      764 HLESCSENGTEYRETVYLN-----STVNSITVYSCGKMAAPTNTCTTGITDPP 818
Db      1391 KMDQVEVFSRKLKESKSLNIMMLVPHKRYLVSIYVQAGMTSEVEDSTITMIDRPP 1450
Qy      819 PDSQPI-----TSVSHSVK--VKSQFEASHGPTKAYVILTTG-----EAGHP 862
Db      1451 P-PPHIRNEKQVILSKSINFTVNCWFSQDNGVKKFYVREADSGDELKEQOHP 1508
Qy      863 SADVLKYTYDDFKGASDTYVYLLIRTEKGRSSQSLSEVLKYEIVQNESTTG----- 916
Db      1509 LPSYLEYRNASIRYQVTV--FASICANPNNSNKS-----FNILGAMESLGKRDPT 1562
Qy      917 ---YNNKLEPIGSRACVAGFTNITFHPQKGLIDGASVYSFR--YSDA-VSLP--- 967
Db      1563 QOKFCGPKPHTAVRISIRAFQ-----LFD--EDLKEFTKPLYSDFSLPTT 1611
Qy      968 -ODPGVIGAVFGCIFGLV---VYGGFIWRKK--RDKAKNNEVSFSQIKP----- 1015
Db      1612 ESEP--LFGALIEVSAGLFLIGMLVAVALLCRKQVSHGRPPARLSIRDRPLSVHL 1669
Qy      1016 -----KSKSLIEVENFEAFKQADNSCGFAEEYEDLKVGISQPKYAAELAEENRG 1067
Db      1670 NLGQKGNRTSGPITKINGEFGHFMLOQDSNVLISKYBELKQVGRNSCDIALPEKRG 1729
Qy      1068 KRRYNNVLPYDISRYKLS-VQTHSTDDYINANYMFGYHSKQFIATQGPLPNTLKDFWRM 1126
Db      1730 KRRYNNILPYDATRKYLSNVDDDDPCSDYINASYIPGNFRREYITQGPLGTQKDFWKM 1789
Qy      1127 VKEKNVVAIIMLTCKVEQGRTCCEZYWPSKO-AQYGDITVAMTSEIPLPMTIRDFTVK 1185
Db      1790 VWEQNVHNIWVTCQVEKGRVKCHYWPADDDSLYTGDLIQMLSESVLPMTIRREFKIC 1849
Qy      1186 NIQISESHPL-RQHFSTMPDHGVPDITDILNFRYLVADYWKOSPPEPSPILVHCSAGV 1244
Db      1850 GEEQDAHRLIRHFHYTWPDHGVETQSLIQFRTVADYINSPGAGPVTYVHCSAGV 1909
Qy      1245 RTGFIADRLILOYENENTDVVGIYVDLMKHPRLMQTEQYVFLNQCVDLIVRSQKD 1304
Db      1910 RTGFIADRLIQQDSDSDYIYGAVHDLRLHVRVMQTEQYVYLAQCVRVILRAKRL 1969
Qy      1305 SKVDLIYQNTAMTIENIAP 1325
Db      1970 RS-----EQENPLFIYENVP 1986

```

RESULT 4

A49724
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type H precursor - human
 N:Alternate names: protein-tyrosine-phosphatase, stomach cancer-associated type 1; SAP-1
 C:Species: Homo sapiens (man)
 C>Date: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C:Accession: A49724
 R:Matcozaki, T.; Suzuki, T.; Uchida, T.; Inazawa, J.; Ariyama, T.; Matsuda, K.; Horita, K.
 J. Biol. Chem. 269, 2075-2081, 1994

A:Title: Molecular cloning of a human transmembrane-type protein tyrosine phosphatase and
 A:Reference number: A49724, MUID:94124561, PMID:8294459
 A:Accession: A49724
 A:Molecule type: mRNA
 A:Residues: 1-1118 <MAT>
 A:Cross-references: UNIPROT:Q15426; GB:DL5049; NID:g475003; PIDN:BA03645.1; PID:g475004
 C:Genes: GDB: PTPRH, SAP-1
 A:Cross-references: GDB:305504
 A:Map position: 19q13.4-19q13.4
 A>Note: highly expressed in colon and pancreatic cancer cells but not in the normal cells
 C:Superfamily: protein-tyrosine-phosphatase, receptor type H; fibronectin type III repeat
 C:Keywords: carcinogenesis; duplication; glycoprotein; phosphoprotein; phosphoric monoest
 F:1-27/Domain: signal sequence #status predicted <IG>
 F:27-110/Domain: fibronectin type III repeat homology <3FNA>
 F:28-1118/Product: protein-tyrosine-phosphatase, receptor type H #status predicted <MAT>
 F:28-761/Domain: extracellular #status predicted <EXT>
 F:116-199/Domain: fibronectin type III repeat homology <3FNB>
 F:205-289/Domain: fibronectin type III repeat homology <3FNC>
 F:296-379/Domain: fibronectin type III repeat homology <3FND>
 F:385-468/Domain: fibronectin type III repeat homology <3FNE>
 F:474-558/Domain: fibronectin type III repeat homology <3FNF>
 F:564-658/Domain: fibronectin type III repeat homology <3FNG>
 F:667-737/Domain: fibronectin type III repeat homology <3FNG>
 F:762-778/Domain: transmembrane #status predicted <TM>
 F:779-1118/Domain: intracellular #status predicted <INT>
 F:846-1070/Domain: protein-tyrosine-phosphatase homology <PP1>
 F:325-78, 83, 107, 132, 149, 172, 196, 203, 286, 304, 312, 329, 352, 376, 383, 401, 436, 439, 470, 490, 558, 5
 F:1022/Active site: Cys (phosphocysteine intermedate) #status predicted
 F:1028/Binding site: substrate phosphate (Arg) #status predicted

Query Match 16.1%; Score 1130; DB 1; Length 1118;
 Best Local Similarity 25.9%; Pred. No. 3, 1e-55;
 Matches 354; Conservative 181; Mismatches 453; Indels 380; Gaps 40;

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Qy      8 ARLPSPG-----LRMALPLLLLRGLCAGTSPSPIDPSVATVAT 53
Db      25 AAPAPNPGHNLIVETQTSSISLSEVP-----DGLDS--QNSNMYVQCT 68
Qy      54 GENDITQSSSTAFHQNQGTGPQVETNSDEGSSGA--NLSLTREGSGNTOGASQ 111
Db      69 GGGGTETTRNT-----TATVTVGLGPGSLYTGSVWWEKGVNSVGT-- 112
Qy      112 KTESSTGSPVPDIKAVSISPTVWILTWKSNDRASBYK--YVVKHKNENEK--TIVVHQ 168
Db      113 -VTATAPNVNRLRVAQAQNSSIALTWEPDPPDQNSTYGVYEGDGRATRBTAH 170
Qy      169 PWCNIT--GLRPATSYFSTTPTGIGMETWGDPRVIVITTEPIVSDLRVALTGVRRAIS 226
Db      171 --TNIYVDGLEPCLYAFSM----- 188
Qy      227 WSNNGTASCRVLLESIGSHEELQ-----DSRLQVNIISDKPQVOYNINPYILQSKTKG 282
Db      189 WVKNGNGNSRETRNATTANPVRKPSGGSDHQLHPEL--GGRWHA-RPTELIDLRTSA 246
Qy      283 DPLTEGGLDASNTBRSRAGSPPAVHDSLVGPVDPSSGQGRDTEVLLVGLPSTRYN 342
Db      247 LEMVAERLETOQTPRS-----PVD-----GLGPGSLVT 275
Qy      343 AITYSQAANTGEPQPAIERTNALQVFDYTVANISATSLITLWKUSDNNESSNNTYTKH 402
Db      276 CSVWEKDVNSSMRLVSTTAPNPNVRLIYEAQNNSSIALTWEPDPPDQNSTYGV 335
Qy      403 VAGETSSNLNVSEPRAVIPLGSSSTFYNTICPVYGLDLEGTPGLQVH----- 451
Db      336 YTDGGR-----GTRSTAHNTITVDR-----EPGLIYFVSVWVKNGKINS 377
Qy      452 -----TPPVDSFRVTVSTTEIGLAWSHDAE-----SPQWHLITQEGAGNSRYEI 498
Db      378 SRETRNATAPNVNRLHMETQNNSSIALCWEVDPQPYQDYTWVGYTGDC--GGIETRN 436
Qy      499 TTNQSIILIGLPPGTGTCETIYPKGNGREGASRYCNRTVSANFDIHVVYVTTTEML 558

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Db      437 TTNTSVTAERLEPELTLYTFSVMAE-KNGARGSRONVSITVPNAVTSLSKODWTNSTIAL 495
Qy      559 DWMSPD--GASEVYVYHL--VIESHGSGNHTSTYKATITLOGLIGTLVNTLISPEVDHW 614
Db      496 RMTAPQGPQSSYSYVWVSWREGMTDPTOSTGTDITLTKLEAGSLYHLVMAERNEVR 555
Qy      615 GDPSTAQYTPSVNSNDVSTNTTAATLSWQNF--DDASPTYSCLLIERAGN----- 666
Db      556 GYNSTLTAATAPNEVTDQNTQTKNSVLMWKAAPGDHSDLYVYVWQMAKGRPRGQD 615
Qy      667 -SSNATGVNTDITGTDATVTELIPGSSYTVVEIPAQVGDGKISLEPRKRSFC--TDPSMA 723
Db      616 PQAMVAVQTSRTNETWYKVEALEPGLYVFMARNDVASSTQ---SLCASTYPPDVT 671
Qy      724 SFDEEVVPEKRALVLTCTCPGANAAPPELEVSAGANNATLIESCSSENGTEYETVYL 783
Db      672 ITSCVSTAGYVNLIMSCPGGYEAFELV-----GGQRSGSDRS----- 712
Qy      784 NFSTSYNISITTVSCGMAAPTRNTCTGTIDPPPDGSPNITSVSHSVKRFSGFEAS 843
Db      713 -----SCGEAVS-----VLGL----- 723
Qy      844 HGPITKAYAVILTTGEBAGHPADVLKTYTDDPKKASDITYYLIRTEEKRSQSLSEVLK 903
Db      724 -GPARYPATITTT-----IWDGKK-----VVS 744
Qy      904 YEIDVGNESITLGYNGKLEPLGSRACVAGFTNITFPQKGLIDGAEVYSFRRYSDA 963
Db      745 HSNVCHTESA----- 754
Qy      964 VSLPQDDGVICGAVFGCIFGALVITVYGFIEMRRKRDANKNEVSFSQIKPKKSKL--- 1020
Db      755 -----GVLAGAVVGL--LFLILVGLLIFPLKRRKKK-----QQRPELRDLVFS 797
Qy      1021 -----IRVENFEAYFKQOADSNGCPABEYEDLKLVGISQPKYAAELANRGNRYNVL 1076
Db      798 SPQDIPADFDADHVRKNERDSNCGPADREYQOLSLVGHSSQMVASASNNAKNRYNVL 857
Qy      1077 YDISRVKLS-VQMTSTDDYINANWPGYHKKDPIATQGPLPNTLAKDWRWVMEKANYAI 1135
Db      858 YDMRSVPLKPRHIEBPGSDYINASFMPGLMSPOEFATQGPLPQTVGDWFLVMEQOSHLL 917
Qy      1136 IMLKCYEGRGRTKEEYWP-SKQADYDITVAMTSEIVLPEMTIRDPETVKNIQTSSEHP 1194
Db      918 VMLNCHGAGRWKCEHWPDLDSQCTGHKLVTLVGEVMEWVYRELLILOVEBQKTL 977
Qy      1195 LRQHFHTSWPDHGVDDTDLINFRYLVDRVMKQSPESPILVHGSAGVGRGTFTAI 1254
Db      978 VRQHHYQAMPDHGVPSSPDTLLAFPMRLRQMLDQMEGSPPIVHCSAGVGRGTTLALDV 1037
Qy      1255 LIYQIENENTVDVYGIYDLPMARPLMVQTEDOYVFLNQCVLDIVRSQ 1302
Db      1038 LLRLQSGEGLIGPSPFVRKMRSESRPLMVQTEAOYVFLHQCICGSSNSQ 1085

RESULT 5
C41214
protein: tyrosine-phosphatase (EC 3.1.3.48), receptor type 10D, long splice form precursor
C:Species: Drosophila melanogaster
C:date: 28-May-1992 #sequence_revision 12-Jun-1992 #text_change 24-Apr-1998
C:Accession: C41214
R:Yang, X.; Seow, K.T.; Bahrl, S.M.; Oon, S.H.; Chia, W.
Cell 67, 661-673, 1991
A:title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sube
A:reference number: A41214; MUID:92034988; PMID:1657401
A:Accession: C41214
A:molecule type: mRNA
A:Residues: 1-1630 <YAN>
A:Cross-references: GB:M60465
C:Genetic8:
A:Gene: FlyBase:Fcpl10D
A:Cross-references: FlyBase:FBgn0004370
C:superfamily: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repe

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C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolyase; recept
F:1197-1213/Domain: transmembrane #status predicted <TM>
F:1197-1213/Domain: intracellular #status predicted <INT>
F:1214-1630/Domain: intracellular #status predicted <INT>
F:1255-1515/Domain: protein-tyrosine-phosphatase homology <PMP>
F:1467/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1473/Binding site: substrate phosphate (Arg) #status predicted

Query Match      14.6%; Score 1028; DB 2; Length 1630;
Best Local Similarity 25.7%; Pred. No. 2,96-49;
Matches 330; Conservative 232; Mismatches 470; Indels 250; Gaps 52;

Qy      119 PPSVFDIKAVSISPTN-VILTKSNDTAASEKYVYKHKE--NEKTTV-VHQPQCNIT 174
Db      405 PLPVRNLRISINDKTNMTLITWEADPASTQDEYRIVVHELETFGDSTLTTRFTLE 464
Qy      175 GLRATVSVSITGIGNETMGDPRIKVTIEPIP--VSDLRVALTVGRKAALSWSNG 232
Db      465 SLPGRVSLSV-QAVKKESENETSIFVYRPSPIEDLSIRMGLN--ISWKS-- 517
Qy      233 TASCRLVESIGSHELTQDSRLQVNSIDLKPGVQVNNIPYLQSNKTKGDPDTEGGLD 292
Db      518 -----DVSKEQ-----QREV-----LVSNGTS 536
Qy      293 ASNTERSRAGSPAPVHDESIVGVPDSSGQOSRDTEVLVGLPEGRYNAVYVSGAANG 352
Db      537 DLRT-----QKTESRLVINKLQGAAYELKVPV-VSHD 569
Qy      353 TEGQPAIEFRITNALIQVDTAVANISATSLTLTKVSDNBSNYYTKIHVAGTDSNL 412
Db      570 LRSEPHAVFOAVVNPNNPMTIETVRNSVYLVHMSPESGFTYSIRYRTDSQWVRL 629
Qy      413 -NVSEPRAVIPGLSSSTFYNTVCVVLGDIAG--TPGFQVHTPPVPSDFRVTVSTEI 470
Db      630 PSVSTEDADITDKKGEKTYIQVNTVSPGVSPVQEVNTTVPNPNSNI-IQLVDSNI 688
Qy      471 GLAMSHD--AESFQMH-----ITQDAGNSRVEITTNOSIIGGLFPGTKCFE 518
Db      689 TLEWPKPEGREVSITLKWMPSDNPGVQTKVNSNKSADLSTVRVLIGELMPGVQYKFD 748
Qy      519 IVPKPGNGTSGASTVCNRTYPSAVPDIHV-----YTTTMMLDKMSPD 564
Db      749 IQTTSYGLSGIT-SLVPRTMPLIQSDVVVANGKEBERDITLSTYPT-----PQ 798
Qy      565 GASEY-VYHL-----VIESHGSGNHTSTYDKATITLOGLIPGLYNTLISPEVDHWMDP 617
Db      799 SSKFPIYRSGGAEIRDEKELANDT--DRKVTGLVGRKLYNIT-----VMTVS 848
Qy      618 NSTAQ-----YTRP-----SNVSNIDVSTNTTAATLSWQNFDPASPTYSCLLIE 662
Db      849 CGVASLPIQRQDRLYPPEITQLAHNTITDTEISLRMLDPKGEVNDFOIAYTLAUNLL--- 905
Qy      663 KAGNSNATQVNTDITGTDATVTELIPGSSYTVVEIPAQV--DGKISLEGRKSFCTD- 718
Db      906 -AQMMTTRNEI-----TISDLRPHRNTFTVVVRSGETSSVLSRSSPLSFTTNE 955
Qy      719 --PASMASF-DCEVVPKEPALVLTCTCPGANAAPPELEVSAGANNATLIESCSSENGTE 775
Db      956 AVPRVERFHFPTDVQPS--INFEWSL-PSEAGVIRQFIAATNINNLTDAGQO---D 1009
Qy      776 YRTETVY-----LNFSTSYNISI--TVSCGMAAPTRN--TCYTGITDPPPDGSPNIT 826
Db      1010 FESSEARGVINKLAPGETVYFKIQAKTALIGG-----PEREVRQMTPLAPRAPTAQVVP 1065
Qy      827 SV--SHNSVKYKF--SGFEASHGPIKAYAVILTTGEAGHPSA-----DVLKTYTDDFK 875
Db      1066 EYVRSSTIQRFRKNYFSDQNGQVRYTIIIVADDKAKNAGSGLMPSPWLVDQSVSV--WL 1123
Qy      876 KGASDITYTVLIRTEEKRSQSLSEVLKYEIDVNEST---TLGYNGKLEPLGSYRACV 932
Db      1124 PYAIDPYIPFENRSEV-----DVTITGENDNHKIGICNGPLSGTTIGKV 1170
Qy      933 AGFTNITFPQKGLIDGAEVYSFRRYSDAVSLPQDGVICGAVFGCIFGALVITVYG 992

```

Db 1171 RREF-----GADKFTD-TAYSFPIQTDQDNTSLIYAI--TVPLTIIIVLVT 1214

QY 993 FIFMRKKR-----KDAK-NNEVSPQIKPKKSKLIRVNEFAVYRKQAOANCGFAEE 1044

Db 1215 LIYKRRNNCRKTKTQDSRANDMWSLPDVIQGNRIILKNFAHRLMSADSDFFSSE 1274

QY 1045 YEDLKLVGISOPKYAAELAEENRGNRYNNVLPYDISRVKLS-VQTHSTDDYINANMPGY 1103

Db 1275 FEELKTVGRDQPCFTFADLPENRPNRFTNLIPYDHSRFLQPDVDDSGSDYINANYVPH 1334

QY 1104 HSKKDFIATOGPLPNTLKDPMRWMEKNYAIIMLTKEVQGRTKCEEYWPSSKQAO-DYG 1162

Db 1335 NSRREFIVQGPLHSTRDDPMRWCMESNSRALVMLTRCEKREKCDQYMPNDVYVFAFG 1394

QY 1163 DITVANTSEIVLPEWTIRDPFTVKNIQTSSEHPLRQFHTSPMDHGVPTTDLINFRYL 1222

Db 1395 DIIVQILNDSHADWMTTEFML--CRGSERILRHFFHTTWDPGVNPQQLVRFVAF 1452

QY 1223 RDMKQSPSPSPILVHCSAGVGTGTFIADRLIYQIENENTVDYVGIYDLMRHPMLV 1282

Db 1453 RD-RICABQRPVIVHCSAGVGTGTFILDRILQIINTSDYVDIPIGIYVARKERVMV 1510

QY 1283 QTEDOYVPLNQCVDIVRSQKD 1304

Db 1511 QTEBOYICIHQCLLAVLBGKEN 1532

RESULT 6

D41214

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 10D, short splice form precursor

C.Species: Drosophila melanogaster

C.Date: 28-May-1992 #sequence_revision 28-May-1992 #ext_change 09-Jul-2004

C.Accession: D41214, A41215

C1:Yang, X.; Seow, K.T.; Bahri, S.M.; Oon, S.H.; Chia, W.

Cell 67, 661-673, 1991

A.Title: Two Drosophila receptor-like tyrosine phosphatase genes are expressed in a sub

A.Reference number: A41214; MUID:9203498; PMID:1657401

A.Accession: D41214

A.Status: nucleic acid sequence not shown; not compared with conceptual translation

A.Molecule type: mRNA

A.Residues: 1-1557 <YAN>

R.Tian, S.S.; Teoulfas, P.; Zimm, K.

Cell 67, 675-685, 1991

A.Title: Three receptor-linked protein-tyrosine phosphatases are selectively expressed c

A.Reference number: A41215; MUID:9203498; PMID:1657402

A.Accession: A41215

A.Molecule type: mRNA

A.Residues: 1-904,'L',906-1125,'Q',1126-1165,'YR',1168-1171,'A',1173-1215,'L',1217-1456,

A.Cross-references: GB:M80538; NID:9158644; PIDN:AAA28952.1; PID:9158645

C.Gene: FlyBase:FBgn0004370

A.Cross-references: FlyBase:FBgn0004370

C.Superfamily: protein-tyrosine-phosphatase, receptor type 4B; fibronectin type III repe

C.Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept

F.1197-1213/Domain: transmembrane #status predicted <TM>

F.1214-1557/Domain: intracellular #status predicted <INT>

F.1285-1515/Domain: protein-tyrosine-phosphatase homology <PPL>

F.1447/Active site: Cys (phosphocysteine intermediate) #status predicted

F.1473/Binding site: substrate phosphate (Arg) #status predicted

Query Match 14.6% Score 1026; DB 2: Length 1557;

Best Local Similarity 25.7%; Pred. No.3-5e-49;

Matches 329; Conservative 233; Mismatches 470; Indels 250; Gaps 52;

QY 119 PPSVFDIAVSIPTN-VILTWKSNDAASEYKVVYKHKME--NEKITYV-VHOPMGNIT 174

Db 405 PLPVRNLSINDDDKNTMIITWEADPASTQDEYRIIVHELETFNGDSTLTTRTFLE 464

QY 175 GLRPAIVSITIGIGETWGDPRVIVITEPIP--VSDLRVALLGVKRAALSWNGNG 232

Db 465 SLLEGRNYSLV-QAVSKKESNETSIFVYTRPSSPIIEDLKSIRMGIN--ISWKS--- 517

5

QY 233 TASCRVLLSEIGSHELTQDSRLQVNIISDLKPGVQYININPILQSNKTKGDPCTEGGLD 292

Db 518 -----DVNSKQE-----QYEV-----LYSRNGTS 536

QY 233 ASNTERSPAGPTAVHDESLVGPVDPSSGOQSDTEVLVGLPGRYRNATVYVSOANG 352

Db 537 DLRT-----OKTESRLVINCLOPGAAYELKVA-VSHD 569

QY 353 TEGQQAIEFTTNALQVFDVAVNISATSLTLIKVSDNESSNYTKIHVAGSTDSNTL 412

Db 570 LRSEHAFVQAVYVNPENRMTIEYRSNSVYLVMHSPESGFEYTSIRYRTDSBOQWRL 629

QY 413 -NVSEPRAVITGLRSTFYNTVTCVYGDITEG-TPGFLQVHTPPVPSDRVYVSTTEI 470

Db 630 PSVSTEDITDMTKGKRTYIQAIVTSFGVESPVQEVNTTVPNPVSNITQLVDSRNI 688

QY 471 GLANSHD--AESFOMH-----ITQEGANSVHEITTNOSIIIGLFPSTKYCFE 518

Db 689 TLEWPKPEGRVESYILKMWPSDNPGRVQTKVNSKNSADLSTVRVLIGELMPGVQYKFD 748

QY 519 IVPKGPNTBEGASTVCNRTYPSAVFDIHYV-----YTTTMMMLDKSPD 564

Db 749 IQTTSYGLISGIT-SLYPRTPMLIQSDVYVANGKEDEBDRTILSYRPT-----PQ 738

QY 565 GASEY-VYHL-----VIESKGSNHTSYDKAITLQGLIPGLYNTTISPEVDHWGDP 617

Db 799 SSKKFDIYRPSGDAELRDKKELANDT--DRKVTFLGVLPGLNINIT-----VWTVS 848

QY 618 NSTLQ-----YTRP-----SNVSNIDVSTNTTAATLSQNPDDASPTYSCLLIE 662

Db 849 GGVALSLPIORODRLYPPIQLAHANITTDREISLRMLPKGEVNDPDIAYLTADNLI--- 905

QY 663 KAGNSNATQVNDIGITDAITVELIPGSSYTYEIFAQVQ--DGKISLEPKKSKCTD- 718

Db 906 -AQMNTTRNEI-----TISDLRPHRYTITVVRSTESSVLRSSPSLASFTTNE 955

QY 719 --PASMASF-DCEVWPKPALVLMKTCPPGANAGFELEVSSGAMNATHLESCESENGTE 775

Db 956 AVPKRVRFPHTDQPE--INFEMSL-PESEANGVIQPSIAYTNINNTLDAGMC---D 1009

QY 776 YRTFVY----INFSTYNIISIT--TVSCGMAAPTRN-TCTTGITDPPPDGSPNIT 826

Db 1010 FESSEAFGVIKNKKPGETVYFKIQAKTALGFG---PERYRQTMPIILAPREPATGVVP 1065

QY 827 SV--SHNSVVKF--SGFEASHGPIKAYAVILTTGAGHPSA-----DVLKYTDDPK 875

Db 1066 EYVRSSSTIQRFRKRYFSDQNGQVMTYITVADKAKASGLEMSWLDVGYSV--WL 1123

QY 876 KASDITYVYTLITTEKGRQSLSLEVLYKEIDVGNST--TLGYNGKLEPLGYSYRACV 932

Db 1124 PYAIDPYPPENRSVE-----DFTIGTENCDNHKIGYCNGLKSGTTIGVAV 1170

QY 933 AGFTNITFPHQNGGLDGAESYVSFSRYSDAVSLPDQPVICGAVGCGCFALVITYVG 992

Db 1171 RREF-----GADKFTD-TAYSFPIQTDQDNTSLIYAI--TVPLTIIIVLVT 1214

QY 993 FIFMRKKR-----KDAK-NNEVSPQIKPKKSKLIRVNEFAVYRKQAOANCGFAEE 1044

Db 1215 LIYKRRNNCRKTKTQDSRANDMWSLPDVIQGNRIILKNFAHRLMSADSDFFSSE 1274

QY 1045 YEDLKLVGISOPKYAAELAEENRGNRYNNVLPYDISRVKLS-VQTHSTDDYINANMPGY 1103

Db 1275 FEELKTVGRDQPCFTFADLPENRPNRFTNLIPYDHSRFLQPDVDDSGSDYINANYVPH 1334

QY 1104 HSKKDFIATOGPLPNTLKDPMRWMEKNYAIIMLTKEVQGRTKCEEYWPSSKQAO-DYG 1162

Db 1335 NSRREFIVQGPLHSTRDDPMRWCMESNSRALVMLTRCEKREKCDQYMPNDVYVFAFG 1394

QY 1163 DITVANTSEIVLPEWTIRDPFTVKNIQTSSEHPLRQFHTSPMDHGVPTTDLINFRYL 1222

Db 1395 DIIVQILNDSHADWMTTEFML--CRGSERILRHFFHTTWDPGVNPQQLVRFVAF 1452

QY 1223 RDMKQSPSPSPILVHCSAGVGTGTFIADRLIYQIENENTVDYVGIYDLMRHPMLV 1282

Db 1453 RD--RICAQRPIVHCSAGVSGTFTTLDRILQIINTSDYVIFGIVAMRKRVMV 1510
 Qy 1263 QTEQDVFLNOCVLDIVRSQKD 1304
 Db 1511 QTEQDVFLNOCVLDIVRSQKD 1532

RESULT 7

S17671

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 22-Nov-1993 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
 C/Accession: S17671; S40287

R/Gdblink, M.F.B.G.; van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.;
 FEBS Lett. 290, 123-130, 1991
 A/Title: Cloning, expression and chromosomal localization of a new putative receptor-lik
 A/Reference number: S17669; MUID:9208644; PMID:1655529
 A/Accession: S17671
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: mRNA

A/Residues: 1-583 <GB>
 A/Cross-references: UNIPROT:Q64497; EMBL:X58289
 R/Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993

A/Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A/Reference number: S40280
 A/Accession: S40287
 A/Molecule type: mRNA

A/Residues: 377-483, 'T', 485-486 <HEN>
 A/Cross-references: EMBL:Z23056; NID:9438149; PID:CA060591.1; PID:9438150
 C/Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re

C/Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot
 F/311-536/Domain: protein-tyrosine-phosphatase homology <TRP>
 F/468/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/494/Binding site: substrate phosphate (Arg) #status predicted

Query Match 14.0%; Score 981.5; DB 2; Length 583;
 Best Local Similarity 39.0%; Pred. No. 2.4e-47;

Matches 226; Conservative 102; Mismatches 191; Indels 61; Gaps 15;

Qy 789 YNISITVSCGKMAAPRTNTCTTITDPPPGSPNI-----TSVSHSVK--VKS6GF 840
 Db 5 YLVSITKQVSGMTSEVVEDSTITMIDRPQ--PPIKRVNEKDVLSKSSINFVNC6WF 62
 Qy 841 EASGPIKAVAVITTG-----EAGPSADVLTITDPPKGAASDTTYTILRTTEK 892
 Db 63 SDTGAAGVFAVVRREADSMDELKPEQHPPLPSYLEYHNASIRVYQTNV--FASKCAES 120
 Qy 893 GRSQSLSEVLYKEIDVGNESITLG-----YNGKLEPLGSRACVAFNTITPHQ 943
 Db 121 PDSSSKS---FNIKLGEMDSLGKCDPSQKFCDCGLPHITVYRISIRAFQIF---- 172
 Qy 944 NKGLIDAESEVSPFSRYSDAVSLPDP--GVICGAVFCIFGALVITVVGIFWKR--K 999
 Db 173 DEDKEFTKPLVSDTPFSPMTTSEPLFGVIEGVSAGFLIGLVALLVAFFICQKQASH 232
 Qy 1000 RKDAKNNEVFSQIKP-----KSKKLIIVENFEAYFRKQOADSNCFAEYE 1046
 Db 233 SREPSRRLSIRRRPLSVHLNLGOKNRKTSCKIKINQFGHFMRKQADSNVLSKYE 292
 Qy 1047 DLKLVGASOPKAAELNENGRNRYNNVLPYDISRVKLS--VQTHSTDDYINANYMPGHS 1105
 Db 293 DLKQVSGSQCDLILPENRGRNRYNNILPYDASRVKLSNVDDPCSDYINASTIPGNF 352
 Qy 1106 KQDIATQGLPLNTLKDFWVWVWKNVYAILMLTKCYEQGRTKCEYVPSKQ--ADYGD 1164
 Db 353 RREYATQGLPLRGTKDFWVWVWKNVYAILMLTKCYEQGRTKCEYVPSKQ--ADYGD 1164
 Qy 1165 TVANTSELVLEPMTITDTPVKNITQTSBHP--RQHFPSWPDHGVPTDILLINFRILYR 1223
 Db 413 ILQVWSSVSLPEWMTIRFVKICSEQLDAHRLIRHFHYVWPDHGVPTDILLINFRILYR 472

Qy 1224 DYKQSPPESELVHCSAGVSGTFTFLAIDRLIYOINENTVDYGVYLDLRLMRPLMVQ 1263
 Db 473 DYINRSPGAGPSVHCSAGVSGTFTFLAIDRLIQLQDSKDSVDYIGAVHDLRLRHHVWQ 532
 Qy 1264 TEDQVFLNOCVLDIVRSQKDLIYQNTAMTIENT 1323
 Db 533 TECQVYVHOCQVDVRSQKDLIYQNTAMTIENT 1323

RESULT 8

A55148

Protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat
 N/Alternate names: OST-PRP; osteoclastic protein-tyrosine-phosphatase
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C/Accession: A55148
 R/Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.
 J. Biol. Chem. 269, 30659-30667, 1994
 A/Title: Identification of a hormonally regulated protein tyrosine phosphatase associated
 A/Reference number: A55148; MUID:95074080; PMID:7527035
 A/Accession: A55148

A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-1711 <MAU>
 A/Cross-references: GB:I36884

C/Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosi
 C/Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III rep
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prot
 F/1-18/Domain: signal sequence #status predicted <SIG>
 F/119-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MA
 F/1174-1398/Domain: protein-tyrosine-phosphatase homology <PRP1>
 F/1350/Active site: Cys (phosphocysteine intermediate) #status predicted
 F/1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 13.6%; Score 957.5; DB 1; Length 1711;
 Best Local Similarity 24.5%; Pred. No. 2.8e-45;

Matches 383; Conservative 227; Mismatches 524; Indels 431; Gaps 72;

Qy 22 PLILL--ILRLGQL-----CA--GNP-----SPIDPSVAT-----VATGEN 56
 Db 3 PLILLALLMLQGLAEDDACSLSGSPDRQGGPLLSVNSHGKSTSLFSLVVALELG 62
 Qy 57 GITQISSTAESFHKQNGTGP--QVETNTSEDS-ESSGANDS-----LRTPEGS 103
 Db 63 GF-----DYALSLRVDSSGSEGOQLAHTNESFEFHGLVPSRYQLKLVLRPCQNV 118
 Qy 104 NGTDGASQKTPSSSTGSPVPEDIKAVSI--SPTNVILTWKSNDAASEYKVVVKKHNEKT 162
 Db 119 TIT-----LTARFAPTVVVGILQLHSAGSPARLEASWSDAFGDQSYQLLYH--LESG-T 170
 Qy 163 ITTVHQPWCNT-----GLRPATSVYPSITPGIGNETWGDPRVIVKI-----TEP 207
 Db 171 LA-----CNVSPDPLSYSPGDLPGTQVLEVI-----TWAGSLHAATSLIOWTEP 218
 Qy 208 IPVSDLEVALTGVAKALMSNGNGTASCRVLIESIGSHELTODSRLOVN---ISDLKP 264
 Db 219 VPPHMLALRALGTSLQAFNNSSEGAITSFHLMLTDLGNTTAVIIGQVSTHFFLHSP 278
 Qy 265 GVQVYNIPYLIQSNKTVG--DPLQTE----- 288
 Db 279 G-----TPHELIKASAGPQIOWPSATETWYPSYSPEDLVLTPLRNEILMSWKAGLGARD 333
 Qy 289 -----GGIDASNT--EESRA--GAPTPAVHD-----ESLVGVD-----PSSGQ 323
 Db 334 GYVLKLSGPMESTITLPEBCNAVFPGLPFGHTTLQKVLAGEYDVMWEGSTVLAESA 393
 Qy 324 QSRD--TEVLLVGL--FGTRYNATVYSQAANGTEGQQAIEFTNALQVDPVAVN 376
 Db 394 LPREVPGARLMDLDELSKQGR--ALIVSDNAPSLG-----N 431
 Qy 377 ISATSLTLIMKVDNESSNTYKIHVAGETDSSNLVSEPRAVIPGLRSTFPNITVCP 436
 Db 432 ISVPS-----GAT-----HVFPGILVPGAHYVDIAS 458


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437 VLGIETGPGFLQVTPPVSDPRV--TVSTTEIGLAW--SSHDASFQMHITQBCAGN 493
459 STGIQSISQ---ISGTSTPLPPOSLEVISRSSEPSDLTIAWGPAGQLEGYKVMHQDSQR 515
494 SRVEIT---TNQSIIGGLPFGTKYCFEIVPKGPN--GTEGASRTVGNRFVPSAVFDIHW 548
516 SPGLVDLGPDTLLSLTKSLVFGSSSYVSAMAMGNLGSQKIHSTRAAPNTLSIGF 575
549 VYVTTTEWMLDMKSPDASEVYVTVLESKSGNSHTSTYKATLQCG--LIPTLYNTT- 605
576 AH--QPAIKASWYHPGGRD--AFHLRLYRL--RPLTLESEKVLPREAQNFVW 623
606 -----ISPEVDHWGDPNSTAQ---YTPRSNVSINIDVSTNT--TAATLISQNDQDAS 652
624 AOLTAGCEFOVQLSTLWGSRRSSSANNMTGPSAPLTVNTSDAPLOLVSAHAPVGR 683
653 PTYSCLLIEKAGNSNATQV-----TDIGITDATTVELLPGSSYVTEIFPAQVGDGI 705
684 SRVQVTLVYQF--STRATATSIMGPKEDGTSFLGLT-----PGTKYKVEIVSMAG-- 729
706 KSLEPGKRSFCTPDASWASFDCEVPRK-----PALV----- 737
730 -----PLVTAANVSAMTYPLIINELLVSNQASAVVNIAWPSGPIGQACHAQLSD 781
738 ---LKWTCP-----PGANAGFELEVSNGAMNATLBSGSSENG---TRF 776
782 AGHLSWEOPKLQGLFMLRLDLPFGHTISWSVRCRAGPIQASTHLVVLSVEGVPEDVLC 841
777 RTEVTVYLN-----STSTINI 791
842 HPRATYILANWMPAGDVCLVVERLVPGGGTHFVQVNTSGALLPMLMPTTSYLL 901
792 SITTVSCGKMAADTRN---TCTGTITDPPPPD--GSPNITSVSHNSVKKFSGFASHP 846
902 SLTVL--GNRSRWSRAVSLVCSAEMHPPELAEPQVELGTGCVYVNRMSFGKDGQ 959
847 IKAYANILITG--EAGHPADVLKTT--YDFPKKASDTVTVYILRT---EEKRSQSLS 900
960 IQVYGIATINMTLQPSREAINWYWDHYRGC--ESFLALFPNPFYDEPAGPRS--- 1015
901 VLKVELDVGN--STLGYNGKLEPLSGACVAGFNITPHPNKGLIDGAEVYVFS 958
1016 ---WTVPGTEDCDNTQEIENGRKSGPQYRFSVAFSR-----LMTPEITLAFS 1062
959 RYSD--AVSLPQDP--GVICAGVFCIFGALVITVGGFIFWR---KKKRDANNVFS 1009
1063 ASEPRASISLAIIPITVWLGAIVGSI--VIVCAVLCLLRWRCLKGPRSEKDGFSK-- 1117
1010 FQIKP---KSKLIRVENFEAFYKQAOBSCGFAEYEDLKVIGISQRYAAELAE 1065
1118 ---LAPYMLMRTHRIPIHFSFQSTYKASAHHQTFQEFELKEVGDOQLRLAEHPDN 1174
1066 RKNKNYNNLIPYDISRVKLSV---QTHSTDDYINANNYRGYHKKDQFATQGLPNTLKD 1122
1175 IKKNYPRVPLPYDHSRVRLTQPGPHS--DYINANNFIPGYSHTQEIATQGLPKLTLED 1232
1123 FMRMWEKNVYAIIMLTVCVQEGRTKCEYWPSCAQ--DYGDITVAMTSEIVLEWTRD 1181
1233 FRLWMEQOVAVIIMLTVMGEMGRVLCHEWPNASTPYTHGITHILAEPRDEMTRE 1292
1182 FTVKNIQTSSEHPLRQFHFTSMRPHGVDPDTDLINFRYLVRDMKQSPSPSLIYVCSA 1241
1293 FOLHGTEGOKORVQLOFTTWPBHSVREABSSSLAFVELVQEOVQATQGGPLVHCSA 1352
1242 GVGRTGTTAIDLILYOIENENTVYVGIIVDLMRHPLWQTEQDYVFLNQCLD--IVR 1300
1353 GVGRTGTTAIDLILRLQLEEKVADVENVYIIRLHRPIMQLTSLQYIPLHSLCKMLLE 1412
1301 SOKDS 1305
1413 GPPDS 1417

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```

RESULT 9
A49502
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type 4E, splice form A precursor - 1
C:Species: Drosophila melanogaster
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: A49502
R:oon, S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 268, 23964-23971, 1993
A:Title: Alternative splicing in a novel tyrosine phosphatase gene (DPRP4E) of Drosophila
A:Reference number: A49502; MUID:94043220; PMID:8226938
A:Accession: A49502
A:Molecule type: mRNA
A:Residues: 1-1767 <ON>
A:Cross-references: UNIPROT:Q9W4F5, UNIPROT:Q24495; GB:L20894
A>Note: authors translated the codon ATA for residue 1715 as Leu
C:Genetics:
A:Gene: ptp4E
A:Superfamily: ptyBase:P8gn0004368
C:Keywords: protein-tyrosine-phosphatase, receptor type 4E; fibronectin type III repeat;
alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor
F:1254-1270/Domain: transmembrane #status predicted <TM>
F:1271-1767/Domain: intracellular #status predicted <INT>
F:1353-1573/Domain: protein-tyrosine-phosphatase homology <PRP>
F:1525/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1531/Binding site: substrate phosphate (Arg) #status predicted

Query Match 13.6%; Score 954; DB 2; Length 1767;
Best Local Similarity 24.5%; Pred. No. 4,7e-45;
Matches 352; Conservative 179; Mismatches 448; Indels 458; Gaps 56;

QY 67 SEHQ--NGTGP-----QVETNTSF-----DGESSGAND-- 94
DB 469 SYHQINASEVPAEPFVALESQITLNTLTEXTLDSLGRRLIAYVALSKGVASNASDIT 528
QY 95 -----SLRTEQG-----SNGTDAQSKTBSSTG----- 118
DB 529 RYTRPAAPLIQELRSIDQGLMSWRSDVNSRODRYEVHQRKGTREKRMATNFSILTH 588
QY 119 ---PSYFDLIKAVSIS-----PNN-----VILTKSNDTAS 147
DB 589 YLHPGSGYEVKVAISHGVASEPHSYFOAVFPKPNQLTQTVHTNLVLIHQABE--GS 646
QY 148 EY--KYVVKHMEKNTITVHQPWCNITGLRP-----ATGVFSI--TPGIGNETW 195
DB 647 DFSEYVVRKYTD-----ASPMQRIQGLHENEKATIKMTYGERILVQVNTVSGVSS- 697
QY 196 GDRPVYKITEPIVSDLEVALTGVKKAALSMWNGNTASC-----RVLLESI 243
DB 698 PHLPLNVTMPQPVSNV--VPLVDSRNLTLFWPRPDGHVDFYTLKMPPTDEEDRVFQNV 756
QY 244 GSHEELTQDSRLQVNTSLDKPGVQVNNINPYLQSKTKGDPGLTGCGLDASTERSRAAS 303
DB 757 TQLEDSLSPS--VRIPLIEDLSPRQYRF-----EYQASSNGIRSGTHLSTRTM 803
QY 304 PTAIVADESLVGPVDPSSGQGRDTEVLVGLER-----GTRNATVYVSOAANGTEGQPA 359
DB 804 PL--IQSDVFLA-----MGHEGQGDETITLSTTPRPASTRDIDYRFSM-----GDP-- 849
QY 360 IERTNAIQVFTVAVNISATSLTIIMKVSDESSSNYYTIKHVAGTDSNLTAVSEBRA 419
DB 850 -----TIKDEKLANDT-----ERKL 865
QY 420 VIPGLRSSTFYNIITVCPVLGDIETGPGFLQVHTPPVSDPRVTVSTTEIGLAWSSIDA 479
DB 866 SFGSLTPGLQNVYVWYWSGVASLIPVQVRVRLHPLSDLKAAQVAREITLHMTAPAG 925
QY 480 E---SPQMHITQKAGNSRVEITTNOSIIIGGLPFGTKYCFEIVPKGPN--GTEGASRT 533
DB 926 EYTDPELQYLSADEBAPOLLQVTFKNTETITLQGRPNYNYFTVYVNASGSLQIGDIPADV 985
QY 534 VGNRTVPAVAPDINHYVYVTTTBMLDMKSPDASEYVYHVLIESKSGNSHTSTYDKAITL 593

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Db      986 VSTLMRSSA--PISASYOTLT-----APPGKVDYFQPSDVQ-----1019
Qy      594 QGLIPGTLNITISEVDHW-----GDNSTRAQYTRPNSNIDVSTNTTAATLSKQNF 649
Db      1020 ---PG-----EYFEWSLEPAEQHGPIDYFR-----ITCQAD 1049
Qy      650 DASPTSYCLIEKAGNSNATQVVTDIGIDATVTELEPGSSYVEIFAQVGDGKISLE 709
Db      1050 DAADVSSIEFPV-----NATQ-----GKIDGLVPNHIIYFRQAQSAAGY-----1089
Qy      710 PGRKSFCTDPASMASFCEVVPKEPALVLKWTCPGANAGFELEVSAGMANNATHLES 769
Db      1090 -----GARE-----HIQ---1097
Qy      770 SENGERTYEVLYNFTSTSYNISTITVSCGMAAPTRNTCTGTGIDPPPGSPNITSVS 829
Db      1098 -----TWPIIAPVPPESTVPLEVS 1117
Qy      830 HNSVVKFS---GFEASHGPIKAYAVILT--TGEAGH---PS-ADVLKYT---YDDE 874
Db      1118 RTSSTIEISFPGQYNSNAHGWASTYIIIAEDVKGIAAGLEMPQDQATVWMLPYQ-- 1175
Qy      875 KKGASDYVYVLIIRTEEKRSQSLEVLKYEIDVGN-ESTTLGYNGKLEPLGSTRACVA 933
Db      1176 ---AIEPYNPFL--TSNGSRKSSL-EASHLTIGTANCDKHQAGYCNGLPAGATTYRIKIR 1229
Qy      934 GFTNTTFHPQKGLIDGASVYSFERYSDAVSLPQ-DGVCIGAFGCIFGALVIVTGG 992
Db      1230 AFTD-----EDKFTDVYSSPTTERSDTVIAATVSAVLAVALVAVV- 1273
Qy      993 FIFPKKKKDAKNNVSEFSQIKPKSKL-----IRVENFAYEKKQADSNCGFA 1042
Db      1274 ---YQHRCQOLIRASKLARQDELALPEGITTRNRVHVXKDESEHRIKMSADDFRS 1330
Qy      1043 EYEDLKLKLVGISQPKYAAELANRKNRYNNVLPDISRVKLS--VQHSSTDYINANTMP 1101
Db      1331 EEFELKLVGRDQACSFAFLPCNRPKNRFTNLLPYDHSRFLQPVDDDDGSDYINANTMP 1390
Qy      1102 GYHKKDRIATQPLRNTLXDPKRWVMEKNYAIIMLKVCYEGCTTKEBWP--SKQAD 1160
Db      1391 GHNSPREFTVTOGPHSTRFEFRWCWESNSRAIYMLTRCFEGEKCDQWYVDRVAMF 1450
Qy      1161 YGDIIVANTSEIIVPEWTRIDFTVKNIQTSSESHPLQFHTSWPHGVPDITDILLINFRY 1220
Db      1451 YGDIKVOILIDTHHDSISEFMS--RNCESRIKHHFTFTWPRGPEPPLSLVRVR 1508
Qy      1221 LVDRYMKQSPESPILVHCSAGVGTGFIAIDRLIYQIENENTVAVYGIYVDMHRRPL 1280
Db      1509 AFRDVI--GDMRPPIIVHCSAGVGRSGTFIALDRILQIHKSDDVDYDIGIVAMKERVF 1566
Qy      1281 MVQTEDDVYVFNQCVLDIVRSOKSKVDLI-----YQNTAMTYENLAPVTTFG 1330
Db      1567 MVQTEQDYVCIHQCLAVLEGEKHLADSLHLANDGYEVT---KTYLEROPQTMG 1620

RESULT 10
B49502 protein-tyrosine-phosphatase (BC 3.1.3.48) receptor type 4E, splice form B precursor - f
C/Species: Drosophila melanogaster
C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: B49502
R/Oon: S.H.; Hong, A.; Yang, X.; Chia, W.
J. Biol. Chem. 266, 23964-23971, 1993
A/Title: Alternative splicing in a novel tyrosine phosphatase gene (DPT4E) of Drosophila
A/Reference number: A49502; MUID:94043220; PMID:8226938
A/Accession: B49502
A/Molecule type: mRNA
A/Residues: 1-1615 <OON>
A/Cross-references: UNIPROT:Q9MAF5; GB:U20894
C/Genetics:
A/Gene: FlyBase:PCP4E
A/Cross-references: FlyBase:FBgn0004368
A/Introns: 1605/3

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C/Superfamily: protein-tyrosine-phosphatase, receptor type 4E, fibronectin type III repe
C/Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept
F:1254-1270/Domain: transmembrane #status predicted <TM>
F:1271-1615/Domain: intracellular #status predicted <INT>
F:1353-1573/Domain: protein-tyrosine-phosphatase homology <PTP>
F:1525/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1531/Binding site: substrate phosphate (Arg) #status predicted

Query Match 13.5%; Score 949; DB 2; Length 1615;
Best Local Similarity 24.5%; Pred. No. 7,8e-45;
Matches 345; Conservative 177; Mismatches 438; Indels 448; Gaps 54;

Qy      67 SFHQ-NGTGR-----QVETNTSE-----DGSSGAND-- 94
Db      469 SYHQTNASRPAPFPVAABEQITNLTETVLDLSLGRRLIAVQALSKVAASASGIT 528
Qy      95 -----SLRPEQG-----SNGTDAQSKTPSSTG-----118
Db      529 RYTRPAAPLIQELSDIGLMLSWRSDVNSRQDREYEVHYQNGTRREKRTMATNETSLTIH 588
Qy      119 ---PSVPDIKAVSIS-----PTN-----VILTKNSDITAS 147
Db      589 YLHPSGTEVVAHISGVSRSEPHSYFOAVPFPQNTLTQVHTNLVLMQAPL-GS 646
Qy      148 EY-KYVVGKMKENKTIIVVHQPCNITGLRP-----ATSYVPSI--TPGIGNETW 195
Db      647 DFSEYVVRKRD-----ASPQIRISGLHENEARIKDMHGERYLVQVNTVSGVES- 697
Qy      196 GDFRVIKYTEPIVSDLRVALTGVRKAALSWSNNGTASC-----RYLLESI 243
Db      698 PHLPLANTMPQOVSNV-VPLVDSRLNLTLEMPRDPDGVDEYTLKMPTEDEDEYEFKNV 756
Qy      244 GSHBELQDSSLQVNIQSLDKRGVQYVNIPIYLOQNKTKGDFLGEGLDASNTERRAGS 303
Db      757 TQLEDSLSPS--VRPIEDLSFGQYR-----EQVASSNGRSSTHLSRTM 803
Qy      304 PTAPEHBSLIGPVPDPSSGQSDTEVLLVGLER-----GTRYNATVYSQAANGEGQPOA 359
Db      804 PL-IQSVFLA---NAGHEQGDFTLLSYTPPADSTRFDIYRFEM-----GDP-- 849
Qy      360 IEFRTNALQVDTAVNISATSLTLIMKVDNESSSNYYKIHVAGETSSNLVSEPPRA 419
Db      850 -----TIKKEKLANDT-----ERKL 865
Qy      420 VILPGRSTFYNTIVCPVLDIGETPGELQYHTPRVPVSDPRVTVVSTTEIGLAMSSDA 479
Db      866 SPSGLTPGKLVNVTWVWSGGVASLPVQRYRHLPLPSIDKAIQVAAERLTLMTAPAG 925
Qy      480 E---SFMHTTQEGAGNSRVEITTNOSIIIGLFPQTKYCFEIVPKGPN--GTEGASRT 533
Db      926 EYTPPELOVLSADEAPQLQONVTKNTEITLQGLRPYHNHYFTVYVNSGSIQGTDFADVS 985
Qy      534 VCNRTVPSAVEDIHVYVYTTTMMWLDWKSPPDGAEEYVHLVIESKHGNSHTSTYDKAITL 593
Db      986 VSTLMRSSA--PISASYOTLT-----APPGKVDYFQPSDVQ-----1019
Qy      594 QGLIPGTLNITISEVDHW-----GDNSTRAQYTRPNSNIDVSTNTTAATLSKQNF 649
Db      1020 ---PG-----EYFEWSLEPAEQHGPIDYFR-----ITCQAD 1049
Qy      650 DASPTSYCLIEKAGNSNATQVVTDIGIDATVTELEPGSSYVEIFAQVGDGKISLE 709
Db      1050 DAADVSSIEFPV-----NATQ-----GKIDGLVPNHIIYFRQAQSAAGY-----1089
Qy      710 PGRKSFCTDPASMASFCEVVPKEPALVLKWTCPGANAGFELEVSAGMANNATHLES 769
Db      1090 -----GARE-----HIQ---1097
Qy      770 SENGERTYEVLYNFTSTSYNISTITVSCGMAAPTRNTCTGTGIDPPPGSPNITSVS 829
Db      1098 -----TWPIIAPVPPESTVPLEVS 1117
Qy      830 HNSVVKFS---GFEASHGPIKAYAVILT--TGEAGH---PS-ADVLKYT---YDDE 874

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Db      1118 RTSSTIEISFROGYFSNAHGVNRSYTIITIAEDVKIASGLGEMPSMDQVQVITWLYQ-- 1175
Qy      875 KKGSADTVYVYLIPTERKGSQSISEVLKYEIDVGN-ESTTLGYNGKLEPLGSRACVA 933
Db      1176 ---AIEEYNPPL--TSNGSRKSSSL-EAEHLITGTANCDDKHQAGYCNCPGAGTYYIKIR 1229
Qy      934 GFTNITFHPONKGLIDAEISVSFSRSDAVSLPQ--DPGVICGAVGCGALVITVYGG 992
Db      1230 AFID-----EDKFDITYSSPITTEKSTTVVAVATVANVLVAVV-- 1273
Qy      993 FIFMRKKRKAANKNEVSFSQIKPKSKL-----IRVNEFAYFKKQOASNCGR 1042
Db      1274 ---YCOHRCQILRRASKLARMODELALPEGYITPMPRYAVKQPSHMYRMSADSPFRS 1330
Qy      1043 EEEYEDLTVGISQPKYAELEAENRGKRNYNVLPYDISRKLS-VQTHSTDDVYINANVP 1101
Db      1331 EEEBELKHVRDQACSPANLPCRRPKRRFTNLPYHRSFKLQPVDDDDSDITANANVP 1390
Qy      1102 GHSHKDFLATQGPLPNTLKDFFRWVWEKNVVAIIMLKVCQEGRTKCEYMP-SKQAD 1160
Db      1391 GHNSPREFIVTQGPFSHTREEFWRMCWESNSRAIVMLTQCFEKGREKCDQVWVDRVAVF 1450
Qy      1161 YGDITAMNSEILPEMTTADFTVYKNIQTSSEHPLQGFPTSPDHGVPDTTDLINFRY 1220
Db      1451 YGDIKVLQIIDTHYHWSISEFWVS--RNCESEIMHFHTWPDPGVDEPPLSLVRFVR 1508
Qy      1221 LVNDYKQSPESPPIIVHSGAGVGTGTFLAIDRLIYQIENENYVNVVYIVYDLRMHRL 1280
Db      1509 AFRDVI--GTDMKPIIVHSGAGVGTGTFLAIDRLIYQIENENYVNVVYIVYDLRMHRL 1566
Qy      1281 MOTEPOYVFLNOCVLDIYRSQKSKVD 1308
Db      1567 MVQTEQOYVCIHQCLAVLEKHEHLAD 1594

RESULT 11
A:56178
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
M:Alternate names: protein-tyrosine-phosphatase BPT-2
C:Species: Homo sapiens (man)
C:Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A56178, S12052; B44929
J:R. Pulido, R. Kneeger, N. X. Serra-Pages, C., Saito, H., Screuli, M.
J: Biol. Chem. 270, 6722-6728, 1995
A:Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.
A:Reference number: A56178; MUID:95204468; PMID:7896816
A:Accession: A56178
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1912 <PUL>
A:Cross-references: UNIPROT:P23468; GB:L38929; NID:9755652; PIDN:AAC41749.1; PID:9755653
R:Kneeger, N. X., Screuli, M., Saito, H.
EMBO J. 9, 3241-3252, 1990
A:Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases.
A:Reference number: S12049; MUID:91006018; PMID:2170109
A:Accession: S12052
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 390-1912 <KRUR>
A:Cross-references: GB:X54133; NID:935789; PIDN:CAA38068.1; PID:935790
R:Adachi, M., Sekiya, M., Ariimura, Y., Takekawa, M., Itoh, F., Hinoda, Y., Imai, K., Yada
Cancer Res. 52, 737-740, 1992
A:Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A:Reference number: A4929; MUID:92119637; PMID:1370651
A:Accession: B44929
A:Molecule type: mRNA
A:Residues: 1756-1804 'C', 1806-1845 <ADA>
A:Cross-references: GB:S78086; NID:9243545; PIDN:AAB21147.1; PID:9243546
A:Experimental source: pre-B cell NALM-6
A>Note: Sequence extracted from NCBI backbone (NCBIN:78086, NCBI:P:78087)

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A>Note: the authors did not report the entire codon for residue 90
C:Genetics:
A:Gene: GDB:PTPRD
A:Cross-references: GDB:131384; OMIM:601598
A:Map position: 9p24-9p24
C:Superfamily: leukocyte antigen-related protein, fibronectin type III repeat homology, 3
ogy
C:Keywords: glycoprotein, phosphoprotein, phosphoric monoester hydrolase, transmembrane p
F:38-100/Domain: Immunoglobulin homology <IMM1>
F:140-209/Domain: Immunoglobulin homology <IMM2>
F:250-304/Domain: Immunoglobulin homology <IMM3>
F:711-811/Domain: fibronectin type III repeat homology <3PR>
F:1293-1912/Domain: leukocyte common antigen homology <3PR>
F:1669-1892/Domain: protein-tyrosine-phosphatase homology <LAC>
F:1553/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1553/Binding site: substrate phosphate (Arg) #status predicted
F:1844/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1850/Binding site: substrate phosphate (Arg) #status predicted

Query Match      12.5% Score 879; DB 2; Length 1912;
Best Local Similarity 24.3%; Pred. No. 8,56-41;
Matches 375; Conservative 209; Mismatches 560; Indels 400; Gaps 67;

Qy      14 SPGLRMALPLLLRLRLGQLCAGTSPPIPDSEVATVATGNGITQISSSTASFKHNG 73
Db      212 SAGTRYSAPAVLYRELREVRVPRRS-IPPTNHEIMPGGSVNITVA----- 259
Qy      74 TGTPO-----VETTSDEGSSGAND-SLRTPEGNSGT-----DGASQKP 114
Db      260 VGSFMPYVKKMLGAEDLTIPDDMPIGRNVLINDVRSANVTCVAMSTLGIVIAIQTIV 319
Qy      115 SSTSPSPVDIKAVSISPTVITLWKSNDTASEYKVVGHKENE---KITTVHQPV 170
Db      320 KAL-PRKPGIPVYESTATISITLWDSGNPEPSY-YIIOKKKNSBELYKEIDGVAITR 377
Qy      171 CNITGLRPATSYVFSITPGINETWGDPR--VIKVIITEPIVVS---DLRYALTGVKKAAL 225
Db      378 YSVAGLSPSYSDYERRVY-ANNVIGRGPSEPVLTQISEQAPSSAPRDVQARMLSTIIV 436
Qy      226 SW---SNGNGTAGSRYLSEISGHELTQSRQVN-----ISLAKGVQY 268
Db      437 QWKEPEEPNQIQ-----GRVYVYMDPTGVNMMKKNVADAQITTLGILVPOKTY 488
Qy      269 NINPYLLQSNKTKGDPLEGTGGLDASNTERRASGSPAPVHDESLGVPDPSGQGSRD 328
Db      489 SVKVLAFTS-----IG-DGLSSDIQVITQVGGQPLNFRFA-----EPES---ET 530
Qy      329 EVLL-----VGLPEGRY-----NATVYSQANGTE 354
Db      531 STLSWTPPRSDTIANYELVYKDGEGEORITIEPGTSYRLQGLKPNLSLYFRLLA---A 587
Qy      355 GQPOALEFRINAIV-----FDYAVNIASTSLTLWK-----VSDNESSNNTY 399
Db      588 RSPQGLGASGTAELISATMGSKSPAPDDISCSPPSSTSLVSKQPPPEVKQGITTEYSI 647
Qy      400 K-IHVAGETDSNLNVSEPR---RAVIPGLRSTFNITVCEVLGDIESTGPGFLQV--- 450
Db      648 KYTAVDGEDDKPHEILIGISDPTKYLLRQLEKMTVEYRIV-TANDVVGSGPESLGLRT 706
Qy      451 --HTPPVPVSDPVPVYVSTTBIGLAMS-----HDAESFQMHITQEGAGNSR----- 495
Db      707 NEDVPGPRKVEAVNVSTSVKSWRSVVPKQHQIRGQVHNHVRMENGEPKQOPMLK 766
Qy      496 -----VEITTNQSLIGLFPGTXYCEIIVPKGPNTEGASRTVCNRTVSAVDP 545
Db      767 DWVLADAQWEPDTEHMDIISGLQPEISYSLTVAITTKG-DGA-----RSKRLVST 819
Qy      546 IHVY-----YVTTEM---WIDWKP----- 563
Db      820 TGAIVPGKPLVINHQQMTALIQMHPVDVTFPGLQYRLKPKRKMDEPLTTLSEFKEDH 879
Qy      564 -----DGASRYVHVLESFGSNHSTYDKATITLQGLPGLTLYNTISPEVDHWGD 616

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Db      880 FTATDIHKGAS-YVFRLSARKVGFGEEMV--KEISIDEEVP-----TGEPQNIHSEG- 929
Qy      617 PNSTAQVTRPSNVSNIDVSTTTTAATLSMGNFDDASPTYSCLILEKAGNSMNTQVYTD 676
Db      930 -----TTSTISVQLSMQ-----PP-----VLAENKGIITKYLTLIR 960
Qy      677 IGI-----TDAVTTELIPGSSYVEIFAQVGGIKSLBGRKS-----FCTDP 719
Db      961 INIPLEMEQLIVADDTMLTLTGAKPDTTYVVKRAHNSK-----FGPSPSVQFTLP 1015
Qy      720 ASMA---SPDCEVPEKPEPALVLTCTCPGANAGLELVSSGAMNATHLESCESENGTEY 776
Db      1016 VDOVFANFHYKAMK--TSVLLSWEIPEANYSAMPFI---LYDDGKMEVEV---DGRAT 1068
Qy      777 RTEVTYNFSTSVNIST---TVSCGMAAPTRNTCTGTIDPPPPGSPNITSVNSV 833
Db      1069 OKLVNKKPEKSYSEVLTNRGNSAGLOHRTAKTADVLTAKPAFIGKTNLDMG---I 1124
Qy      834 KYKFSGEASHGPIKAYAVIL-----TTGEAGHPSADVLKTYDDPKKASDTYVYLIR 888
Db      1125 TVQLEPVPANEN-IKGYIITIVPLKSRGKIKRWESPDMEDELKEISRK-----R 1178
Qy      889 TEKGRSQSLSEVLKYEIDVGNESITLG---YNGKLEPLGSYRACVAGFTNITFHPQNK 945
Db      1179 SIRYGREVELKPYIAAHFDVLPTEFTLGDDKH-----GGFT-----NK 1217
Qy      946 GLIDGASYSYF-----SRYS-D-AVSLRDP-----GYI--CGAVFG 979
Db      1218 QLOSGOE-YVFFVLAWEHESKMYATSPYSDPAVSMDLDPITDEBEGLIWVGPLYA 1276
Qy      980 CIFGALIVTVGGRIFPRKCKKADKNNVSPSQIK-----PKSKLIRVENFPA----- 1028
Db      1277 VVFICIVIAI---LYKRAESDSKRSIIPNNKEIPSHHPTDPVELRLNFTPGMAS 1333
Qy      1029 -----YFKKQADNSCGFAEEYEDLKLVGISOPKXAEALENGRNRYNVLV 1077
Db      1334 HPPILELADHIERLKANDELKFSQYESID-PGQGFTEHNSMLVNNKPKRNYANVAY 1392
Qy      1078 DISRYKLS-VQTHSTDYIYANNTMPGYSKDDFIATGCPRLNTLKTQFPRMMEKNVAIL 1136
Db      1393 DHSGVLLSALIEGLPSDYVYNNAYIDGRKONAYIATGSLPETFGDFRMIMEGRSATV 1452
Qy      1137 MLTCVGEQGRTKCEYMPKSKOAOYDGTIVAMTSEIVLPEWTIRDFTVKNIQTSSEHPLR 1196
Db      1453 MMTLEERSKRYKCDQYPSRKTETHGLVQVTLTLVELATYCVTFPALYKNGSSEKKEVR 1512
Qy      1197 QFHTSPDHGVPDPTDLLINFRYLVDYMKQSPPEP-PILVHCSAGVGTGTFIAIDRL 1255
Db      1513 QFGTAMPDHGVPHPHPTPLAF---LRRVKTCPNPDGAPMVVHCSAGVGTGTFIVIDAM 1569
Qy      1256 IYQIENENTVDVGIYVDLRMHRFLMOTEDQYVFLNOCVLDIV 1299
Db      1570 LERIKHEKTYDIYGHVTLMPRAQRNMYVOTEDQYIFIDALLEAV 1613

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RESULT 12

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T14328
protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type, Gmcl precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14328
R/Wright, M.B.; Hugo, C.; Saifert, R.; Distcheche, C.M.; Bowen-Pope, D.F.
J. Biol. Chem. 273, 23929-23937, 1998
A/Title: Proliferating and migrating mesangial cells responding to injury express a novel
A/Reference number: Z17986; MUID:98395110; PMID:9727007
A/Accession: T14328
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Releases: 1-2302 <MRI>
A/Cross-references: UNIPROT:O88488; EMBL:AF063249; NID:G3300095; PID:G3300096; PIDN:AAC3
A/Experimental source: strain wistar
C/Genetics:
A/Note: PTRRO

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C/Keywords: phosphoric monoester hydrolase
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-2302/Product: protein-tyrosine phosphatase receptor type, Gmcl #status predicted <M
Query Match 12.3%; Score 864; DB 2; Length 2302;
Best Local Similarity 23.5%; Pred. No. 7.9e-40;
Matches 405; Conservative 216; Mismatches 533; Indels 568; Gaps 77;
Qy      87 GESSGANDS---LRTPEGSGNGTDGASQKTPSSNGPVPVDIKAVISPTNVLITW----- 139
Db      648 GESSLSEENDIFVATPED-----EPES---SPQ-DVQYTVSPSELRKMSPE 692
Qy      140 KSNDDAASEKYVYKHK---MENEKITVYVHQPWCNITGLRAPATSYVFTP---GIG 191
Db      693 KPNGLIIIA-YEVLQNADLTFVKNKTSITDII-----ISDLKPYLVNIGISRYTRLGHG 745
Qy      192 NETWG--DPRVYKITEPIP--VSDLRVALTGKAAALMSNGNG-TASCVLLESIGSH 246
Db      746 NQSSSLSVSTSETPVPSAPENITVKNISGGEIISFLPRSPNGIIOKTYIYLRNSH 805
Qy      247 BELT-QDSRLQVNIISDLKPGOVNINPYLLQSNKTKGDPITGEGGLDASMTERRAGSP 305
Db      806 EARTINTTSLQITGGLKTYHYIE--VSASTLKEG--GINSRPSILTEADPSP 860
Qy      306 APVDESLVG-----PVDP-----SSGQOSRDEVLV--GLBPGTR 340
Db      861 QNPSVKQLSGVTWLSQWPLEPENGILLYYTVYWDKSLRAINATBASLVSLDYNVD 920
Qy      341 YNAVYSQAAANGT-EGQPOAIEFTNAIQVF---DYTAVNISATSLTIW----- 386
Db      921 YGACVTAFTSTFGDNARSSIIINFRTPEGEPSDPPNDVHYVLLSSSSIIILFWTPVKENG 980
Qy      387 -----KYSDNESSE----- 395
Db      981 IQYYSVYQNTSGTFVQNFLLQVTKESDDVYASARIYLAIFSYTFWLTASTSVNGN 1040
Qy      396 -----NYTK-----INVAGETDS-----NINVSER 418
Db      1041 KSSDIHVTYDQDIPBEPVGNLTPESISSTAHNSWEPSPQPNGLVYYLSLNTQSPPR 1100
Qy      419 AVIP-----GLRSTFYNTVCPVLGDIESTPGF---IQVH-----T 452
Db      1101 HMIPPLTYENSIDFDLLEKTYDIYFKITP---STEGKSESYTTQLHKTEDVDPDT 1155
Qy      453 PPRVPSDFRTVYVSTTEIGLAMS---SHDASFGMHTQESAGSRVEITNOSIIIGL 509
Db      1156 PPI-INTEK--NLSSTISLSWDPPLKPNGAILGHLTLQGPANHTFVTSNGHIVLEEL 1212
Qy      510 PPGTKYCFEIVPKGPNGTGEGASRTVCNRTVPSAVF---DIHVYVYTTTEMLDMK--SP 563
Db      1213 SPFTLYSFFPAARKMKGL-GPSSILFFYTDESAPLAPQNLTLINTYSDFWLWMSFSL 1271
Qy      564 DGASEYVYHLVIESKHSNHTSYDKAIT-----LQGLPGTLNITTSPEVDHWGD 616
Db      1272 PGGIWKVYSFKI---HEHETDVYFYKNISGLQTDAKLEGLEPVSYSVASAFTKVGNGN 1328
Qy      617 PMS-----TAQYTRPSNVSNID-VSTNTTAATLSMGNFDDASPTYSCL--LIEKAGNS 668
Db      1329 QYSNVVEFTTQESVPEAVNRNIECVARDMOSVAVM---DPRKNTGIIIMHTVIGNS- 1384
Qy      669 NATQVMTDIGTDA--TVTELIPGSSYVEIFAQVGGIKSLBGRKSPCTDPASMASFD 726
Db      1385 -----TKVSRDPTTYFTKLDPMTSYVFEVRASTAGS---EGNSRC-DISTLP--- 1429
Qy      727 CEVVPKEPALV-----LMTCP----- 743
Db      1430 -ETVPSAPTVNAFVNGVSTATLTWKPDITFGFYQYKITTLQRAQKCEMEBECEIEH 1488
Qy      744 -----PG----- 745
Db      1489 QKDQYLYEANTQETBELTGLKKFRWYRPOVAASTNVGYSNASEWISTGTLPEPPDPGPPBNV 1548
Qy      746 ---ANAGFELEVSAGMN-----NATHLESCESENGTEYRTE 779

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      1549 HVAATSEFGINIS--WSEPAVITGPTFLIDVKSVDDEDFNISFLKS--NEENKT---TE 1601
      780 VTINSTSVNIST-----TVCGMAAPTRNTCTTGIDTPP----- 818
      1602 INNLEFTRYSVITTFVGVNSAAYVDKSSAAVITTTLESVKDPDNNMTPOKIPEDEV 1661
      819 -----PDGSPN-----ITSVSHNSVKKFGSGFEASHG- 845
      1662 KFOITLFPSPQNGNIRVQALVYREDPTPAQVHNFSIIQKDTSTIIIMLEGLKGGHY 1721
      846 PIAAYAVILTTGAGHPSADVLTYYTD-----DFKGAADTYVYILIR- 888
      1722 NISVAI-----NSAGAGPKVQKRITMDIAPAPKSKPIPIDATGKLIVSTTITIRMP 1777
      889 -----TEKGRSOSLSEVLKKEIDVNGES-----TTGYN-----GCL 922
      1778 ICYVNDHGPRIRVQVLAETAQOD-GNVTYMYDAYFNKAPRYFNESGFPNPECTEGT 1836
      923 EPLGSYRACVAGFTNTTFHPQNK-----GLIDGASVY-----SFSRYSDAV- 964
      1837 KESGNEIYVIGADNACMI-PGNEBKICNGPLKPKQYLFKPRATNWQGFDTSEYSDPIK 1896
      965 -----SLPQDPGVICAGVFCIGALVTVV-VGGTFPMKKRK-----DAKNEVSF- 1010
      1897 TLGEGLSERTVEIISVTLCTIISITLGTAFAPVARIKQKQEGGTSPRDAEIIDTYFK 1956
      1011 -----SQIKPKSKLIRV-----ENFEAYPKQAOADNCGFAEYEDKLIV 1051
      1957 LDQITVADLELKDELTLLSYRKSIRKISKSPLOHVEICTNSNLKFOESEL--- 2013
      1052 GISQPKYA-----AELAEKGRKYNVNLDPYDISRYKLSVQTH-STDDYINANYMGY 1103
      2014 ---PFTLDLSSTDADLPWNRKAPFPPIKPYNNRVKLIDAVSLPCSDYINASYSGY 2069
      1104 HSKQFIATQGPLPMLTKDFMFWMEKKNVYALIMLTKVCEQGRTCCEWTP--SKQADY 1161
      2070 LCPNEFIATQGPLPGLTVGDFMFWMETRKTIVMLTQCEKGRIRCHQYWPEDNKPTVTF 2129
      1162 GDIYVAMSEIVLPEMTIRDTFTVKNIQTSSEHPLRQFHTSPWDHGVDDTDLINFRYL 1221
      2130 GDIVITKLMEDIQIDMTIRDLKIE--RHQDCMTVAQCNPFTGMEHGVENITPLIHFKYL 2187
      1222 VPDYKQSPESPPIVHGSAGVGRGTFFAIDRLIYQIENENTVDYGIYDLMRHPLM 1281
      2188 VR--TSRAHDTTPMVVHCSAGVGRGVFALDHLTQHINNHPVDIYGLVALSERMCM 2245
      1282 VQTEDQYFLNQCLDIVRSQKSKVDLIYONTTAMTYENL 1323
      2246 VQNLAQYIFLHQCIIDL-SNKGSHQVPCFVNVSTLQMDSL 2286
  
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RESULT 13
 A:protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type O precursor - human
 N:Alternate names: GLEPP1; glomerular epithelial protein 1
 C:Species: Homo sapiens (man)
 C>Date: 03-Oct-1995 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
 C/Accession: A57064
 R:Wigdals, R.C.; Wigdals, J.E.; Goyal, M.; Wharram, B.L.; Thomas, P.E.
 Genomics 27, 174-181, 1995
 A:Title: Molecular cloning of cDNAs encoding human GLEPP1, a membrane protein tyrosine p
 ne to human chromosome 12p12-p13.
 A:Reference number: A57064; MUID:95394455; PMID:7665166
 A/Accession: A57064
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1188 <WTG>
 A:Cross-references: GB:U20489; NID:g885925; PID:AAA82892.1; PID:g885926
 C:Genetics:
 A:Gene: GDB:PTPRO
 A:Cross-references: GDB:454477; OMIM:600579

A:Map position: 12p13.3-12p13.1
 C:Superfamily: protein-tyrosine-phosphatase, receptor type O; fibronectin type III repeat
 C/Keywords: glycoprotein; kidney; phosphoprotein; phosphoric monoester hydrolase; recept
 F1-29/Domain: signal sequence #status predicted <SIG>
 F130-819/Domain: extracellular #status predicted <EXT>
 F130-109/Domain: fibronectin type III repeat homology #status atypical <FN3B>
 F116-409/Domain: fibronectin type III repeat homology #status atypical <FN3A>
 F1329-409/Domain: fibronectin type III repeat homology #status atypical <FN3B>
 F1432-520/Domain: fibronectin type III repeat homology <FN3C>
 F1529-619/Domain: fibronectin type III repeat homology <FN3D>
 F1631-714/Domain: fibronectin type III repeat homology <FN3F>
 F1722-804/Domain: fibronectin type III repeat homology <FN3G>
 F1812-1188/Domain: fibronectin type III repeat homology <FN3H>
 F1812-876,877-1188/Product: protein tyrosine phosphatase phi, long form #status predicted <PHL>
 F1820-844/Domain: transmembrane #status predicted <TM>
 F1845-1188/Domain: intracellular #status predicted <INT>
 F1902-1188/Product: protein tyrosine phosphatase phi, cytosolic form #status predicted <P>
 F1934-1156/Domain: protein-tyrosine-phosphatase homology <PTP>
 F175,154,189,201,227,278,287,323,370,461,490,700,712,733,790/Binding site: carboxydr
 F1108/Active site: Cys (phosphocysteine intermediate) #status predicted
 F1114/Binding site: substrate phosphate (Arg) #status predicted

Query Match 12.1%; Score 854; DB 1; Length 1188;
 Best Local Similarity 28.0%; Pred. No. 1e-39;
 Matches 279; Conservative 158; Mismatches 347; Indels 212; Gaps 41;

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      452 TPVPVPS-----DPRVTVSTTEIGLAMSMDA-----ESTQMTQGAAGNRYEIT 499
      271 TPEIPSGNISGMPDENFSDYETTSQPYWWDASAAPSEDEFEVSVLPMYENNSTLSET 330
      500 TNGSIIIGLFPKTKYCFEIVPKGPNTEGASRTVCNRTVPSAVFDIHV----- 548
      331 EKSTSGSFSPFPVGMILTWLPKPRPTAFD-----FHHIREENFTBYLM 376
      549 VYVTTTMDLWKSPDCASEYVTHLVESRHSNHTSYDKAITLQGLPGLYNTITSP 608
      377 VDEBAHFVAELKEP---GKYKLSVTFPSSSGSCETKRSQSAKSL-----SFYISP 424
      609 EVDHMGDPNSTAQYTRPSVNSINDVSTNTATLSW---QNFDDASPTYSCLIEKA 664
      425 SGE--WIEELT---EKQVHS--VHVLSTT--ALMSTTSQENYNTIVSV-VSLTQCKQ 475
      665 GNSNN-ATQVVTDIGITDATVTELIPGSSYTVEIFAQVGDGKISLEPGRKSFCTDPASMA 723
      476 KESQRLKQCYCTQVNSKPIIENLVPGAQYQVYIARKGPLI-----GPPS--DVTFA 527
      724 SF-----DCEVKEP-ALVTKTCTP--PGANAGFELFVSGAAMNATHESGSENGTEY 776
      528 IVPGLKIDMLVPLGPTAVVLSWTRPYLGVRKYVEMF--YFNPAI---MTSEWTTY 581
      777 RTEVYTLNFSST-----YNISITVSCGMAAPTRNTCTG---ITDPPPPDG 821
      582 EIAAT-VSLTASRIANLPRMYNFRVMTWGD---DELSCDSSTISPTIAPV----- 633
      822 SPNITSVSHNSVKYKS-----GFEASHGPIKAVAVI-----LTGEGAGH 861
      634 APEITSEYKFNLSLITSWTGYDDTDLSSRLMHWVAVGKKIKKSVTRNMVTAIISL 693
      862 PSADVLTATYDDEPKKASPTVYTLRTS----- 890
      694 PPDIDTNLSTACTGESSNTSMRLVKLPAPKSLFAVANKTQTSVTLTLMVEGVADFFE 753
      891 -----EKGRSOSLSEVLKKEIDVGNESSTLGYNGKLEPLGSYRACVAGFTNTTFHPQNG 946
      754 VFCQVQSSGQKTK--LQEPVAVASHVTL-----SLLPATAINCSVTSSH----- 798
      947 LIDGASYSFSRYSRAVSLPDDPGVTCAGVFCIGALVITYVGGTFPMWRK-----RK 1001
      799 ---DSPSVPTFLAVSTMTV--EMNPNVNVVISALITLIGLLVTLILIRKKHQLQMARE 854
      1002 DAKNNEVSFSQIKP-----KSKSL---IRVENFAYPKKQAOADNCGFAEY 1045
      855 CQAGTFVNPASLERDQKLPYNNKNGKGLTNFVQDDFDAYITKMAKSDYKFSIQF 914
  
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Qy	1046	EDLVLVIGSOPKVAAEALENGGKRNRYNNVLPYDISPKYL--SVQHSHTDDYINAMMYGHH	1104
Db	915	BELKILIGDILPHFADLPILNCRKRYNITILPYDSRRLVLSMNEEGADITINAYITIGYN	974
Qy	1105	SKQPIATQGBLPNTLKDPMRWMEKNVAYAILMLTKVCEQGRITXCEEYWP--SKQADQYGD	1163
Db	975	SPQEIATQGBLPETRNDFPMFMVVLQOKSQIIVMLTQCNEKKRVKCDHYWPTPEPIAYGD	1034
Qy	1164	ITVAMTSIYVPEWTIDPVTYKNIQTSSEHRLQPHFSWPDHPV--DTTDLLINRYL	1221
Db	1035	ITVMISEEODDACHRFIRLN--YADMQDVMEHNTAMPDGHVPTANAESTLLOLVHM	1092
Qy	1222	VRDVMKOSPPESPILYIHCSAGVGRGTGTFTIALDRILYQIOTENENTVDVGIYDLMEHRPLM	1281
Db	1093	VROQATKS--KGPMLIHCSAGVGRGTFTIALDRLLQHRDHEPFDILGLVSEKMSYMSM	1150
Qy	1282	VQTEQYVFLNQCV--LDIVRSQDSDKYDLTYQNTT	1315
Db	1151	VQTEQYVFIHQCVQVLMWKKKQDFCISDVIYEVNS	1186

[illegible]

Db	138	--LBEIHYPEKXNVFTVNIISYWGKAFRTMLYKDFPKKTVFNMHMLPGICYSITITQVL	195
Oy	277	SNKTF--KQDPLGTEGGLDASNTERSRAQSPFAPVHDESLVGPVDPSSGOOSRDETVLLVG	334
Db	196	SEAFPNKSTLVEYSG--VSHERPQOHTAPPP-----RNI5V1VN	234
Oy	335	LEPQRTYNATVY5OANGTEGO-----FOALERTNAIQVFDYAVN1SATS	382
Db	235	LN-----KNMWEQSGSPFESEFMRSPEITIE--KDRIF-----	265
Oy	383	TLIKVSDNESSMYTKIHVAGBTD5SNLVSPRAVIFGLRSTSYN1TVCPLDIE	442
Db	266	-----HFEETPEPSSGIS-----S	280
Oy	443	GTPEGLQVHTPPVPSDFRVTVVSTTEIGLAWSSHDA-----ESFQMHITQEGANSRVE	497
Db	281	GWP-----DPSNDYTTISQPYWMBDASATPSEDEDFEVLPHREYNNTTIS	327
Oy	498	ITTNQSI11IGGLFPGTKYCEFIYEKGPNGTEGASRTVCNRTVPSAVFDIHVVYTTIEMW	557
Db	328	EAEKTPAPFSGFPVQIMLSWLPKPKPTAFDG-----PHIH---IEREENF	370
Oy	558	LDKMSPD-GASEYTHLVIESKH-----GSNHTSYDKAITQGLRGI--LYN	603
Db	371	TEYSTVEEAHEFAELKEPEKXYL5VTTPSASGSCETRBSQASKSIFYISPGEMIEE	430
Oy	604	ITISPEVDHWGDNSTAQYRTPSNV5NIDVSTWTTAATLSW-----ONFDASPTYSYCL	659
Db	431	LTERQ--HV-----SVHLASTT-ALMSWTSQENYNSTIVSV-VSL	469
Oy	660	LIERAGNSN-ATQVNTDIGITDATVTELLIPGSSYVEI5PAQVDG1KSLBEPKKSCTD	718
Db	470	TCQOKESQRLKQYCTQVNSSKRI1ENLVPAQYQVVMYLKRGPLI-----GPPS--D	521
Oy	719	PASNASF-----DEVVPKEP-ALVWKPTG-PAANGFELEVS6AMNNA7HLESQSE	771
Db	522	FVTAIAPVPTGIKMLPLPGTAVLVSWTRBYLGVFRKYVEMF--YFNPAT---MTSE	575
Oy	772	NGTEYRTVEVTLNFTS-----YN5ITTV5CGKMAAPTRWTCCTG---ITDP	816
Db	576	WTTYYEIAAT-VSLTASVRLANLLPAMYNYNPRVMTWGD---PELSCDBSSTISFITAP	631
Oy	817	PPPDGSPNITSVSHNSVYKFS-----GPEASHGPIKAYAVI-----LTT	856
Db	632	V---ABEIT5VEYFNSLVI5WTVGDDTDL5H5RMLHMVVA5EGKKIKK5VTRVMT	687
Oy	857	GEAGHP5ADVLKTYDDPKKASSTYTYTLIRT-----EKGR	894
Db	688	AILSLP6DIDYINLSVTACTERGSNT5MLRVLKLEPAPKSLFAVNKTOTSVTLLMVEGV	747
Oy	895	S-----QSL5EVLK5EIDVGN5ESTLGVYNGKLEPLG5YRACVAGFTNITHPQ	943
Db	748	ADFEFVEFCQVSGLEFTELQ5PVAVSSHVTT-----SSL5PATYNC5VTSFSH-----	797
Oy	944	NKGHIDGAE5YVSFSRY5DAV5L5QDQGVICGAVFGCIPGALVTVTVG5GFI5MRKK---	999
Db	798	-----DSP5VPTI5AV5TWTV-EMNNVV5V5L5AL5TL5ILL5VTL5IIRK5HLM	850
Oy	1000	-RKDAKNN5V5FSQIKP-----KKS5TL-----IRVEN5EAYFKQOADSNGCFA	1042
Db	851	AREGAGCFVNF5AL5ER5D5GLPYN5K5NGK5KRK5L5TPVOQD5DA5YIKMAK5D5YFS	910
Oy	1043	E5E5EDTLK5V5G5QK5V5A5EL5A5NN5G5KR5YNNV5LY5DI5RYK-LSVQ5H5T5D5Y5N5AN5MP	1101
Db	911	LQ5E5ELK5IG5D5IH5F5AAD5PL5NCK5KRYN5L5I5Y5DS5R5K5ALL5M5NE5B5G5AD5Y5N5AN5IP	970
Oy	1102	GY5HK5D5FIATQ5GLP5NTL5KD5FM5M5WE5KN5V5AL5IM5LTK5CV5Q5RT5CE5E5YMP-SKQ5AD	1160
Db	971	GY5NP5Q5E5I5AT5Q5GLP5ET5R5D5FM5G5V5L5Q5QS5Q5M5V5ML5TQ5CK5K5R5V5K5DH5Y5M5P5TE5B5IA	1030
Oy	1161	YGD5ITV5M5TS5IVL5P5WT5IRD5FTV5K5IQT5ESH5LRQ5PH5T5SW5D5H5V--DTT5DL5NF	1218

Db 1031 YGDITVEMTISEEDODMHRHFRIN--YADEMODVHFNVTAMPDGHVPTANAESILQF 1088
 QY 1219 RYLVRDMKOSPESPILVHCAGVGRTEFTFIALDLIYOIEMENVDVYGIYDLRMER 1278
 Db 1089 VHVNRQOATKS--KGMIIHCAGVGRTEFTFIALDLIYOHIRHEHFDVLILGVSEKRSYR 1146
 QY 1279 PLMVOTEDOVFLNQCV--LDIVRSQKDSKVDLIYQNTT 1315
 Db 1147 MSNVOTEEQYFIHQCVQIMMMKKQOFCISDIVIENVS 1185

RESULT 15

S60613
 Protein-tyrosine-phosphatase (EC 3.1.3.48) U2 precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S60613
 R:Seimiyu, H.; Sawabe, T.; Inazawa, J.; Tsuruo, T.
 Oncogene 10, 1731-1738, 1995
 A>Title: Cloning, expression and chromosomal localization of a novel gene for protein ty
 A/Reference number: S60613; MUID:95273089; PMID:7753550
 A/Accession: S60613
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1216 <SEI>
 A:Cross-References: UNIPROT:Q16827; EMBL:248541; NID:9963058; PIDN:CAA8425.1; PID:93630
 C:Superfamily: Protein-tyrosine-phosphatase, receptor type O; fibronectin type III repes
 C:Keywords: phosphoprotein, phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:529-626/Domain: fibronectin type III repeat homology <3PR>
 F:962-1184/Domain: protein-tyrosine-phosphatase homology <TPPI>
 F:1136/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1142/Binding site: Substrate phosphate (Arg) #status predicted

Query Match 11.9%; Score 839; DB 2; Length 1216;
 Best Local Similarity 24.2%; Pred. No. 7.3e-39;
 Matches 333; Conservative 200; Mismatches 449; Indels 394; Gaps 57;

QY 134 NVILWKSNDTAASEKYVYK-----HKMENKTIIVVHQP--WCNITGLRPTSIV 183
 Db 39 NIVVLEASDVISPAVVVVKITGESKNVFEEFEFNSTLPPVIFKASVHGL-----YYI 94
 QY 184 FSITGIGNETWGDPRVIVITEPIVPSDLRVALVGVKKAALSMNGNGTASCRVLESI 243
 Db 95 ITLVVVNGVNVTKPRSRITVTKPLPV----- 122
 QY 244 GSHEELTQDSRLQVNISDLK---GVQYNIINPYLLQSNKTKGDPLEGEGGLDASNTERS 299
 Db 123 -----SVSITVDYKPSPEFGVLFEIH-YPEKYNVFRVNIISYWGKDPRTM--- 166
 QY 300 RAGSPFAPVHDSLVGPDPSSGQSRDEVLVGLFEGTRYNATVYQAAANGTEGQFOA 359
 Db 167 -----LYKDFEFG-----KTVFNHMLPGMCCYNTTFQLVCEATFNKSTV 205
 QY 360 IEF-----RTNAI--GVFDVAVNISATSLTLMKVSNDNESSNYTKIHVAGET 407
 Db 206 VEYSVSHPEPKHRAFPNPONISIRIVNLKNK---WE---EQSANFEESPMNSOD 257
 QY 408 DSSNLNVSEPRAVIFGLRSSTFYNTVCPVLGDIETGFGFLQVHTPPVVS-----DF 460
 Db 258 T-----IKEKLFHPT-----EETPEIPSGNISGMDF 286
 QY 461 RTVVSTTEIGLAWSHDA-----ESFQMHTQEGAGSRVEITNQSIIIGLFPRTKY 515
 Db 287 NSSDYETTSQPYWWSASAPSEDEFPVSILPMEYENNSTLSETEKSTGSGSFPPVOMI 346
 QY 516 CFEIIVKGPNGTEGASRTVCNRVPSAVFDIHV-----VYVTTTMLDMKSPD 564
 Db 347 LTMLEPKRPTAFD-----FHIHIREENFTYIMVDEBAHFVALEKRP- 391
 QY 565 GASEVTVLHVLESKAGSNHISTYDKATLQGLIPGLLYNITISPEVDHWGDPNSTAQYT 624
 Db 392 --GKYKLSVTTTSSSGSCETRKSSAKSL-----SFYISPSGE--WIEELT---E 434

QY 625 RPSNVSNIDVSNNTAATLSW-----QNPDDASPTYSYCLLIERKAGNSN-ATQVTPDIGI 679
 Db 435 KPOHVS-FHVLSSIT-ALMSWTSSQENNSTIVSV-VSLTCQKQKESQRLKQYCTQVNS 491
 QY 680 TDAVTELIIPSSSYVEIFAQVGDGIKSLBPRKRSFCTDPASMASF-----DCEVVEKEP 734
 Db 492 SKPIIENLVPAQVQVVIYLRKPLI-----GPPS---DPVTFALVPTGIDKMLLYLGP 543
 QY 735 -ALYKATCP-PGANAAGELEVSSGAMNNAHLESCESSSENGTEVRYTYLNTS----- 788
 Db 544 TAVVLSTWTPPLGVFRKVVEMF--YFNPAF--MTSEWTTYEIAAT-VSLTASVRIA 596
 QY 789 -----YNISITVSCGKMAAPTRNTCTTG-----ITDPPDPSQNTISVSHSVKVF 837
 Db 597 NLLRWMTNFRVNVMTGDD--PELSCDSSSTFITAIV---APEITSVETNSLIYI 649
 QY 838 S-----GFEASHQPIKAVAVILTTGBAGHSADVLKTYVDPEFKGAS----- 879
 Db 650 SMVYGGDDTTDLSHSRMLHMMVV--TEGK-----KKIKSVTRVMTAIIISLP 695
 QY 880 -DTVTVLIRTEERGRQSLSVLKYR-----IDVGNSTTLGYN----- 919
 Db 696 GDTVNLSTVCTCTEGRSNTSMRLRYKLEPAPPKSLFANVKTQTSVTLMVVEGVADPEKVF 755
 QY 920 -----GKLEPLGSTRACVAGFTNITFHQKGLIDGAESEY 954
 Db 756 FQHGSSQKTKLQSPVAVSHVVTISSLRATVSGVTFSSH-----DSPSV 803
 QY 955 VSPERYDAVSLPDDPGVITGAVFGCTEGALVIVTVGGFIEMRK----- 999
 Db 804 PTFIAVSTWVT-EMNPVNVVIVSLALISTLLIGLIVTLIIIRKHLQMARCEGAGTFAN 862
 QY 1000 -----RKDAK-----NNEVSFSQIKP-----KSKL---IRVEN 1025
 Db 863 CASIERGKTPYCNCRSIFAFPLTILPSCMTWTPPLAFYINPMKNGIKRKLTPVOLD 922
 QY 1026 FEAYFKQADSNCGFAEEYEDKLTVGISQPKYAABLAENRGKRYNNVLPYDISRVKL- 1084
 Db 923 FDAYIKDMADSDYKFSLOPEELKLGDIHFRAADLPINRCGRNTNIIIPYDFSVRLV 982
 QY 1085 SVQTHSTDDYINNANMYGHSKODFIATQGPRLNTLKDFRMYMEKNVYAIIMLTICVEQ 1144
 Db 983 SMNEEGADYINANYIPGVNSPOEYIATOGPLDETNRNDFKWKVLQOKSOIIVMLTCCNEK 1042
 QY 1145 GRTICEEYMP-SKQADYGDITVAMTSEIVLPMTIRDFTVKNIGTSSESHPLRQFPTSM 1203
 Db 1043 RRYKCHVWPFTEPIAYGDIYEMISEEDODMACNHRIN--YADEMODVHFNVTAM 1100
 QY 1204 PDHGVF--DTTDLINFRYIVRDYMKOSPESPILVHCAGVGRTEFTFIALDLIYOIEN 1261
 Db 1101 PDHGVPTANAASIIQFVHVNRQOATKS--KGMIIHCAGVGRTEFTFIALDLIOLHIRD 1158
 QY 1262 ENTVDVYGIYDDLHMRPLMVOTEDOVFLNQCV--LDIVRSQKDSKVDLIYQNTT 1315
 Db 1159 HEFVDIILGVSEKRSYRMSNVOTEEQYFIHQCVQIMMMKKQOFCISDIVIENVS 1214

Search completed: May 10, 2005, 19:05:40
 Job time : 69 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:46:26 ; Search time 203 Seconds
(without alignments)
3372.659 Million cell updates/sec

Title: US-09-516-728A-4
Perfect score: 7030
Sequence: 1 MKPAREARLRPPRSGLRWA.....TIYENLAPVTFGKNGYIA 1337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7023	99.9	1337	1	PTPJ_HUMAN
2	4510.5	64.2	1238	1	Q12913; Q15255; Q8NHM2; Q8K3Q2 mus musculus
3	4508.5	64.1	1238	1	PTPJ_MOUSE
4	4499.5	64.0	1216	2	Q62864 ratu
5	4483.5	63.8	1238	2	Q8C1W9 mus musculus
6	2784	39.6	539	2	Q6P4H4 homo sapien
7	2752.5	39.2	1406	2	Q9W6V5 gallus galli
8	2184	31.1	425	2	Q9NPR5 homo sapien
9	1847	26.3	361	2	Q61373 mus musculus
10	1259.5	17.9	1998	2	Q8C1W2 mus musculus
11	1242	17.7	1997	1	PTPJ_HUMAN
12	1239	17.6	1956	1	Q6MZP6
13	1219.5	17.3	1102	2	Q8BUN7 mus musculus
14	1176.5	16.7	1115	2	Q8HDA3 homo sapien
15	1130	16.1	1118	2	Q15426 homo sapien
16	1046.5	14.9	1631	2	Q86N9 mus musculus
17	1043.5	14.8	1556	2	Q8IR87 drosophila
18	1043.5	14.8	1631	1	PTPJ_DROME
19	1043.5	14.8	1962	2	Q9VYU1 drosophila
20	993.5	14.1	579	2	Q9J107 mus musculus
21	991.5	14.1	1705	2	Q9ERK5
22	990.5	14.1	1705	1	PTPJ_MOUSE
23	969	13.8	1607	2	Q9W4F5
24	964	13.7	1607	2	Q8IRSO
25	956	13.6	1711	1	PTPJ_RAT
26	955	13.6	1767	2	Q24495
27	922	13.1	1064	2	Q8SXB2
28	906	12.9	958	2	Q8BIW7 m mus muscu
29	879	12.5	1912	1	PTPJ_HUMAN
30	864	12.3	2302	2	Q8B488 ratu
31	853.5	12.1	1198	2	Q9J1U0 mus musculus

32	852	12.1	1267	2	Q98945 gallus galli
33	849.5	12.1	1216	2	Q62797 ratu
34	846	12.0	1896	2	Q9IAJ1 xenopus lae
35	842	12.0	1187	2	Q28613 crycologus
36	841	12.0	1226	2	Q7TSY7 mus musculus
37	839	11.9	1216	1	PTPJ_HUMAN
38	834.5	11.9	1226	2	Q9ERN5 mus musculus
39	826	11.7	1894	2	Q64487 mus musculus
40	822.5	11.7	1788	2	Q9IAJ0 xenopus lae
41	817	11.6	1367	2	Q20120 caenorhabdi
42	808.5	11.5	1887	2	Q9QK67 ratu
43	807	11.5	1898	2	Q64604 r protei
44	806.5	11.5	1898	2	Q9EQ17 mus musculus
45	804	11.4	1948	1	PTNS_HUMAN

ALIGNMENTS

RESULT 1
PTPJ_HUMAN STANDARD; PRT; 1337 AA.
ID Q12913; Q15255; Q8NHM2;
AC 01-NOV-1997 (Rel. 35, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta)
DE (HPTP eta) (Protein-tyrosine phosphatase receptor type J) (Density enhanced phosphatase-1) (DEP-1) (CD148 antigen).
GN Name=PTPJ; Synonyms=DEP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX MEDLINE=95024024; PubMed=7937872;
RA Oestman A., Yang O., Tonke N.K.;
RT "Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced with increasing cell density.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9680-9684(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95086212; PubMed=7994032;
RA Honda H., Inazawa J., Nishida J., Yazaki Y., Hirai H.;
RT "Molecular cloning, characterization, and chromosomal localization of a novel protein-tyrosine phosphatase, HPTP eta.";
RL Blood 84:4186-4194(1994).
RN [3]
RP SEQUENCE OF 33-1337 FROM N.A., AND VARIANTS COLON CANCER CYS-214 AND PRO-276
RC TISSUE=Colon;
RX MEDLINE=22084388; PubMed=12089527; DOI=10.1038/ng903;
RA Ruivenkamp C.A.L., van Wezel T., Zanon C., Stassen A.P.M., Vlieck C., Casko T., Kluwe A.M., Tripodi S., Petrakis A., Boerlijter L., Groot P.C., Lindeman J., Mool W.J., Meijer G.A., Scholten G., Dauterive H., Paces V., van Zandwijk N., van Ommen G.J.B., Demant P.;
RT "PTPJ is a candidate for the mouse colon-cancer susceptibility locus Sccl and is frequently deleted in human cancers.";
RL Nat. Genet. 31:295-300(2002).
RN [1]
RP FUNCTION: May contribute to the mechanism of contact inhibition of cell growth.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: N- and O-glycosylated.
CC -1- DISEASE: Defects in PTPJ are found in cancers of colon, lung, and breast.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -1- SIMILARITY: Contains 3 subfamily.
CC -1- SIMILARITY: Contains 9 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC -1- DATABASE: NAME=PROJ; NOTE=CD guide CD148 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/row/cd/cdi48.htm".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U10886; AAB36687.1; -;
 DR EMBL; D37781; BAA07035.1; -;
 DR EMBL; AF387844; AAM69432.1; -;
 DR EMBL; AF387823; AAM69432.1; JOINED.
 DR EMBL; AF387824; AAM69432.1; JOINED.
 DR EMBL; AF387825; AAM69432.1; JOINED.
 DR EMBL; AF387826; AAM69432.1; JOINED.
 DR EMBL; AF387827; AAM69432.1; JOINED.
 DR EMBL; AF387828; AAM69432.1; JOINED.
 DR EMBL; AF387829; AAM69432.1; JOINED.
 DR EMBL; AF387830; AAM69432.1; JOINED.
 DR EMBL; AF387831; AAM69432.1; JOINED.
 DR EMBL; AF387832; AAM69432.1; JOINED.
 DR EMBL; AF387833; AAM69432.1; JOINED.
 DR EMBL; AF387834; AAM69432.1; JOINED.
 DR EMBL; AF387835; AAM69432.1; JOINED.
 DR EMBL; AF387836; AAM69432.1; JOINED.
 DR EMBL; AF387837; AAM69432.1; JOINED.
 DR EMBL; AF387838; AAM69432.1; JOINED.
 DR EMBL; AF387839; AAM69432.1; JOINED.
 DR EMBL; AF387840; AAM69432.1; JOINED.
 DR EMBL; AF387841; AAM69432.1; JOINED.
 DR EMBL; AF387842; AAM69432.1; JOINED.
 DR EMBL; AF387843; AAM69432.1; JOINED.
 DR HSR; 138670; 138670.
 DR HSR; P18052; 138670.
 DR GeneW; HGNC:3673; PTPRJ.
 DR MIM; 600925; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR GO; GO:0007163; P:transmembrane receptor protein tyrosine kin. . .; TAS.
 DR InterPro; IPR003361; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR000387; TYR phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00041; fn3; 6.
 DR Pfam; PF0102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTPHPTASE.
 DR SMART; SMO0060; FN3; 8.
 DR SMART; SMO0194; PTPC; 1.
 DR PROSITE; PS00853; FN3; 9.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
 DR Disease mutation; Glycoprotein; Hydrolase; Protein phosphatase;
 DR Repeat; Signal; Transmembrane.
 FT SIGNAL 1 35 Potential.
 FT CHAIN 36 1337 Protein-tyrosine phosphatase eta.
 FT DOMAIN 36 975 Extracellular (Potential).
 FT TRANSMEM 976 996 Potential.
 FT DOMAIN 997 1337 Cytoplasmic (Potential).
 FT DOMAIN 119 205 Fibronectin type-III 1.
 FT DOMAIN 207 291 Fibronectin type-III 2.
 FT DOMAIN 271 364 Fibronectin type-III 3.
 FT DOMAIN 365 452 Fibronectin type-III 4.
 FT DOMAIN 453 538 Fibronectin type-III 5.
 FT DOMAIN 540 620 Fibronectin type-III 6.
 FT DOMAIN 622 717 Fibronectin type-III 7.
 FT DOMAIN 720 811 Fibronectin type-III 8.
 FT DOMAIN 816 902 Fibronectin type-III 9.
 FT DOMAIN 1065 1337 Protein-tyrosine phosphatase.

FT	ACT_SITE	1239	1239	Phosphotyrosine intermediate (By similarity).
FT	CARBOHYD	72	72	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	82	82	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	93	93	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	104	104	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	142	142	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	172	172	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	192	192	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	231	231	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	258	258	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	278	278	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	342	342	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	351	351	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	376	376	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	391	391	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	396	396	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	413	413	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	431	431	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	501	501	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	525	525	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	536	536	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	582	582	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	603	603	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	618	618	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	628	628	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	637	637	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	666	666	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	669	669	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	761	761	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	772	772	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	784	784	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	790	790	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	824	824	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	910	910	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	937	937	N-linked (GlcNAc. . .) (Potential).
FT	VARIANT	214	214	R -> C (in colon cancer; somatic mutation).
FT	VARIANT	276	276	/FTID=VAR_015905. Q -> P (in colon cancer; somatic mutation; dbSNP:1566734). /FTID=VAR_015906. G -> D (in Ref. 1). YNGKLEPLGSRV -> LOWEAGTSGLLP (in Ref. 2). SEQUENCE 1337 AA; 145926 MW; E6752D521C4B6AFE CRC64;
FT	CONFLICT	261	261	Query Match 99.9%; Score 7023; DB 1; Length 1337; Best Local Similarity 99.9%; Pred. No. 0; Matches 1336; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
FT	CONFLICT	918	929	
FT	SEQUENCE	1337 AA; 145926 MW; E6752D521C4B6AFE CRC64;		
Qy	1	MDPAREARLPSPSPGLRMLPLLLLRGLGAGTSPPIPDSPVATVANGENGITQ	60	
Db	1	MKPAREARLPSPSPGLRMLPLLLLRGLGAGTSPPIPDSPVATVANGENGITQ	60	
Qy	61	ISSTASFKHONGTGPVEVTNTSEDESSGANDSLRTPDGSNGTGDASOKTPSSSTGPS	120	
Db	61	ISSTASFKHONGTGPVEVTNTSEDESSGANDSLRTPDGSNGTGDASOKTPSSSTGPS	120	
Qy	121	PVFDIAVAVSIPNNVLLTKSNDTASFKYVVKHMEKETTIVHGWNCITGIRPAT	180	
Db	121	PVFDIAVAVSIPNNVLLTKSNDTASFKYVVKHMEKETTIVHGWNCITGIRPAT	180	
Qy	181	SVFSTIPGIGNETWMDPRIVIKITPIPVSDLRVALTGVRKAALSMNGNGTASGRVLL	240	
Db	181	SVFSTIPGIGNETWMDPRIVIKITPIPVSDLRVALTGVRKAALSMNGNGTASGRVLL	240	
Qy	241	ESIGSHBELTQDSRLQVNTSDLPKGVQVINIPYLLQSNKTKDPLGTGEGDASNTGSR	300	
Db	241	ESIGSHBELTQDSRLQVNTSDLPKGVQVINIPYLLQSNKTKDPLGTGEGDASNTGSR	300	
Qy	301	AGSPFAPVHDESLVGVVDSSGQGSQSDPTVLLVGLFEGRRVNAVYYSOANANGTEGQPAI	360	
Db	301	AGSPFAPVHDESLVGVVDSSGQGSQSDPTVLLVGLFEGRRVNAVYYSOANANGTEGQPAI	360	

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QY 361 EFRFNAIOVDTAVNISATSLTLMKVSNDNESSNTYKIHVAGETDSSNLNVSEPAV 420
Db 361 EFRFNAIOVDTAVNISATSLTLMKVSNDNESSNTYKIHVAGETDSSNLNVSEPAV 420
QY 421 I PGLRSTFYNNITVCPVLGDI EGTGFLQVHTPPVPSDFRVTVSTTEIGLAWSHDAE 480
Db 421 I PGLRSTFYNNITVCPVLGDI EGTGFLQVHTPPVPSDFRVTVSTTEIGLAWSHDAE 480
QY 481 SFOHMTGEGAGNSVEITTNOSIIIGLFPETKTCFEIIVPGRNGTGA STVONRTP 540
Db 481 SFOHMTGEGAGNSVEITTNOSIIIGLFPETKTCFEIIVPGRNGTGA STVONRTP 540
QY 541 SAVFDIHVVYTTTMMMLDMKSPDGA SEVYHLVIESKHGSHNTYKAITLOGLIGT 600
Db 541 SAVFDIHVVYTTTMMMLDMKSPDGA SEVYHLVIESKHGSHNTYKAITLOGLIGT 600
QY 601 LYNITISPEVDHVMGDPNSTAQYTRPSNVSNIDVSTNTTAATLSMNFDDASPTVSYCL 660
Db 601 LYNITISPEVDHVMGDPNSTAQYTRPSNVSNIDVSTNTTAATLSMNFDDASPTVSYCL 660
QY 661 IEKAGNSSNATQVTDIGITDATTVELIPGSSYTEIFAQVGDGKSL EPRKSCCTPA 720
Db 661 IEKAGNSSNATQVTDIGITDATTVELIPGSSYTEIFAQVGDGKSL EPRKSCCTPA 720
QY 721 SMASPDCEVPEPALVLMKTCPPGANGFELEVS SGAMNATHL ESGSENGTEYRTEV 780
Db 721 SMASPDCEVPEPALVLMKTCPPGANGFELEVS SGAMNATHL ESGSENGTEYRTEV 780
QY 781 TYLNFSTSYNISITTVSCGKMAAPTRNCTTGITDPPPDGSPNITSVSHSVKXFGSGF 840
Db 781 TYLNFSTSYNISITTVSCGKMAAPTRNCTTGITDPPPDGSPNITSVSHSVKXFGSGF 840
QY 841 EASHGPICAYAVIILTTGERAGHSADV LKTTYDFFKGSADTYVYTLIRTEEGRSQSLSE 900
Db 841 EASHGPICAYAVIILTTGERAGHSADV LKTTYDFFKGSADTYVYTLIRTEEGRSQSLSE 900
QY 901 VLKKEIDVGNESSTLGYNGKLEPLGSRACVAGFTNITFHPONGKLDGAESEYFSRY 960
Db 901 VLKKEIDVGNESSTLGYNGKLEPLGSRACVAGFTNITFHPONGKLDGAESEYFSRY 960
QY 961 SDAVSLPODPGVICGAVFGCIFGALVITYVGGFIFWRKKRKDKAKNEVSFSQIKPKSKL 1020
Db 961 SDAVSLPODPGVICGAVFGCIFGALVITYVGGFIFWRKKRKDKAKNEVSFSQIKPKSKL 1020
QY 1021 IRVENFEAYFKKQADSNCGFAEYEDLKVGISQPKTAAELAE NRKGRYNNVLPYDIS 1080
Db 1021 IRVENFEAYFKKQADSNCGFAEYEDLKVGISQPKTAAELAE NRKGRYNNVLPYDIS 1080
QY 1081 RVKLSVOTHSITDDYINANVMPGYSKDFIATOGGLPMTLKDFMRMWEKXNYAIIIMLT 1140
Db 1081 RVKLSVOTHSITDDYINANVMPGYSKDFIATOGGLPMTLKDFMRMWEKXNYAIIIMLT 1140
QY 1141 CVEQGRTCCEYWPSPKQADYDITVAMTSEIVLPEWTRIDFTVKNIO TSSEHPLROHF 1200
Db 1141 CVEQGRTCCEYWPSPKQADYDITVAMTSEIVLPEWTRIDFTVKNIO TSSEHPLROHF 1200
QY 1201 TSMWPHGVBDTDLINFRYLVADYMKOSPSPSPILVHCSAGVGTGFIADRLIYOIE 1260
Db 1201 TSMWPHGVBDTDLINFRYLVADYMKOSPSPSPILVHCSAGVGTGFIADRLIYOIE 1260
QY 1261 NENTVDVYGIYVDL EMBRPLMWOQTEDOYVFLNOCVLDIVRSOKDKVLLIYONTAMTY 1320
Db 1261 NENTVDVYGIYVDL EMBRPLMWOQTEDOYVFLNOCVLDIVRSOKDKVLLIYONTAMTY 1320
QY 1321 ENLAPVTTEGKNGYIA 1337
Db 1321 ENLAPVTTEGKNGYIA 1337
RESULT 2
Q8K3Q2 PRELIMINARY; PRT; 1238 AA.
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AC Q8K3Q2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
ID PTPRJ.
GN Name=Ptprj;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ST5;
RA van Wezel T., Ruijvenkamp C.A.L., Zanon C., Stassen A.P.M., Vlcek C.,
RA Csikos T., Tripodi N., Groot P.C., Dauverse H., van Ommen G.J.B.,
RA Demant P.; (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039232; AAK98640.1; -.
DR HSSP; P18052; 1YPO.
DR MGD; MGI:104574; Ptprj.
DR GO; GO:0005615; C:intracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0007507; P:heart development; IMP.
DR GO; GO:0001570; P:vasculogenesis; IMP.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; Tyr phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00041; fn3; 6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SMO0060; FN3; 7.
DR SMART; SMO0194; PTPc; 1.
DR PROSITE; PS00853; FN3; 5.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydroxylase.
SQ SEQUENCE 1238 AA; 136772 MW; 0D02F5F8E23C0B2 CRC64;

Query Match 64.2%; Score 4510.5; DB 2; Length 1238;
Best Local Similarity 67.2%; Pred. No. 3.6e-247;
Matches 901; Conservative 108; Mismatches 226; Indels 105; Gaps 12;

QY 1 MKPAAREARLPBRPGKRWALPLLLRLQLIICAGTSPRPDPSSVATATGENGITQ 60
Db 1 MKPAARETRTPRBRPGKRWALPLLLRLQGVLCAGAPNP----- 43
QY 61 ISSTAEPHKONGTGPQVETNTSEDGSGANDSLRTPGSGNGTDGASQKTPSSTPS 120
Db 44 ----- 43
QY 121 PVFDIKAVISPTNVILTWKSNDRASRYKYVVKHKNENKTIYVHQPNCNITGLRPAT 180
Db 44 --FDIEAV-VAPTSVILTWKNDGASGSCR--IENKESNLTFPVKQNTSCNITGLSPGT 98
QY 181 SVYSITIGIGNEMTGDPRVAKVITEPIPVSDLEVALTGAKKALMSWNGGTASCRVLL 240
Db 99 SYTSIIISVTNETLTK-----TITTEPVPVSDLHVTSGVQARLTWNNAGTASVRLMI 154
QY 241 ESIGSHEELTQDSRLQVNIIDLKPCGVQYINIPYLL-QSNKTKGDLATEGGLDASNTERS 299
Db 155 EELTHS-----SVNISGLKQGTN---NTFAPEBSENEQADPAVAEEVPDANGTKRI 203
QY 300 RAGSPTAFVHDESLVGPVDPSSGQOSRTEVILVGLBGTRYNATVYSQAANGTEGQFQA 359
Db 204 PVTNLSQP-HKNSLAS-VDPSPGQDPSLTETILLTDLKEDTQYNATVYSQAANGTEGQPRN 261
QY 360 IEFRFNAIOVDTAVNISATSLTLMKVSNDNESSNTYKIHVAGETDSSNLNVSEPA 419
Db 262 KVFKTNSIOVSDVPRMNISSASMTLTMKSNYDGSRTSIIVYKIHVAGGTHSVNQTWKEA 321
QY 420 VIPGLRSTFYNNITVCPVLGDI EGTGFLQVHTPPVPSDFRVTVSTTEIGLAWSHDA 479
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Db	322	IIIGLSSTLYNTVHFFLGQTBETPFGLQVYISPDQVSPFRATNVSTRAIGLAMSND	381
QY	480	ESFQMHITQAGAGNSRVEITTNOSIIIGLFPKTKCFEIVPKGPNGBASRTVCRTV	539
Db	382	KSEFEIFKODGGEKHRNASTGNOSYWEVDLKPQTSYHFEIIPRGPDQTBELSTVAGSD	441
QY	540	PSAVEDIHHVYVYVTTETMWLDMKSPDQASEVYHVLVRSKGS-NHSTYDKATITLGLIP	598
Db	442	PSAVTDLRVNVISTTEMQLMONTDDASGYTHLVESKSGSIIIRNNSQKMTTQSLRP	501
QY	599	GLTYNITISPEVDVHWGDPNSTAQYTRPSNVNSIDVSTNTATLTSMONPDASPRYSYC	658
Db	502	GLTYNWTIFPEVDQIQGISNISIQYTRPSSVSHIENVNTTTTAAIRKMKEDTASAYAS	561
QY	659	LLEKAGNSNAIQVVT-DIGITDAVYTELIPGSSYTVVEIFAQVGDGIKSLBGRKSFCT	717
Db	562	VLLIKTGDDGNSVTSNFKQPSI--DIPELIPVSYTVKLTIQVGGDTTSLVPGMTLFC	618
QY	718	DPASMASPDEEVVPEKBPALVLTAKTQCPGAGAGELSEVSGAMNANHISCSSEXTXR	777
Db	619	EPSSVYSFHEEVVPEKBPALVLTAKACFPQMTGTELGVRSDSMNTRLEKCSDDTEGR	678
QY	778	TEVYTNFSTSYNISITVWSCGMAAPRNTCTGTITDPPPDGSPNITSVSHNSYKVF	837
Db	679	TEVAYNFSTSYNISITATLSCGKMAAPQNICTTGITDPTPDGSPNITSVSHNSYKVF	738
QY	838	SGEASHGPIKAAVAVILTTGEASHPADVLKTYVDDPKKAGASTYTYTLIRBEKRSQS	897
Db	739	SGEASHGPIKAAVAVILTTGEAOPADVLKTYEDPKKAGASTYTYTLIRBEKRSQS	798
QY	898	LSEVLKYEIDVGNESFTLLGYNGKLEPLGSRACVAGFTNITPHPONKGLIGASYSYF	957
Db	799	LSEVLKYEIDVGNOSTLLGYNGRLTEPLGSRACVAGFTNITVNLQNDGLINGDSYSYF	858
QY	958	SRSDAVSLPDPBGVTCGAVFGCIPGALVIVVYGGTIFPKRKTKDAKNNVSPQIKPKK	1011
Db	859	SPYSEAVFLPDPBGVTCGAVFGCIPGALVITVYGGTIFPKRKRTAKNNVSPQIKPKK	918
QY	1018	SKLIRVENEAAVFKKQADQNSCGFAEEYEDLKVLSQPKYAAELAENRGNRYNNVLPY	1077
Db	919	SKLIRVENEAAVFKKQADQNSCGFAEYEDLKLIGLSLPTKTAELAENRGNRYNNVLPY	978
QY	1078	DISRYKLSTQVTSSTDYINANVMPGHSKKDPIATQGP.LNTLKQFMRWMEKNVYAITM	1133
Db	979	DISRYKLSTQVTSSTDYINANVMPGHSKKDPIATQGP.LNTLKQFMRWMEKNVYAITM	1038
QY	1138	LTRCVOEGRTKEEYVPSKQADYGDITVAAVMESEYLPMTTTRDFFVKNLQVSESHPIRQ	1197
Db	1039	LTRCVOEGRTKEEYVPSKQADYGDITVAAVMESEYLPMTTTRDFFVKNLQVSESHPIRQ	1099
QY	1198	FHFTSWPDHGVPDPTDILLNFRILYVRDYMKQSPSPSPILVHCSAGVGTGFIAIDRLIY	1257
Db	1099	FHFTSWPDHGVPDPTDILLNFRILYVRDYMKQIPSPSPILVHCSAGVGTGFIAIDRLIY	1158
QY	1258	QIENENTVADVYGIYVLDLRMRPLMOTEOVYELNQCULDIYRSQSKDLYIYONTTAM	1317
Db	1159	QIENENTVADVYGIYVLDLRMRPLMOTEDQYVFLNQCULDIIRAQDSKVDLIYONTTAM	1218
QY	1318	TIYENLAPVTTFGKTNGYIA 1337	
Db	1219	TIYENLEPVSMEGKTNGYIA 1238	
RESULT 3			
PTP_MOUSE			
AC	064455;	STANDARD;	PRT; 1238 AA.
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Protein-tyrosine phosphatase eta precursor (EC 3.1.3.48) (R-PTP-eta) (HHRP Delta-like tyrosine phosphatase) (Protein-tyrosine phosphatase		

DE	receptor type J (Susceptibility to colon cancer-1).	
GN	Name=PtpJ; Synonyms=Byp, Sccl1,	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RA	[1]	
RF	SEQUENCE FROM N.A.	
RC	STRAIN=MRL-LPR/LPR;	
RX	MEDLINE=96140699; PubMed=8549806; DOI=10.1016/0014-5793(95)01415-2;	
RA	Kuramochi S., Matsuda S., Matsuda Y., Satoh T., Ohnogi M.,	
RT	Yamamoto T.;	
RT	"Molecular cloning and characterization of Byp, a murine receptor-type	
RT	tyrosine phosphatase similar to human DEP-1."	
RL	FEBS Lett. 378:7-14(1996).	
CC	-1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein	
CC	tyrosine + phosphate.	
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	-1- TISSUE SPECIFICITY: Expressed in every tissue examined.	
CC	-1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.	
CC	Receptor class 3 subfamily.	
CC	-1- SIMILARITY: Contains 8 fibronectin type III domains.	
CC	-1- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; D45212; BAA08146.1; .	
DR	PIR; S68700; S68700.	
DR	HSP; P18052; 1YFO.	
DR	MED; MG1:104574; PtpJ.	
DR	GO; GO:0007507; P:heart development; IMP.	
DR	GO; GO:0001570; P:vasculogenesis; IMP.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR008957; FN_III-1ike.	
DR	InterPro; IPR000387; TYR_phosphatase.	
DR	InterPro; IPR00242; TYR_pp.	
DR	Pfam; PF00041; fn3; 6.	
DR	Pfam; PF00102; Y_phosphatase; 1.	
DR	PRINTS; PRO0700; PTPPHPTASE.	
DR	SMART; SMO0194; PTPc; 1.	
DR	SMART; SMO0853; FN3; 7.	
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.	
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.	
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.	
DR	KW Glycoprotein; Hydrolase; Protein phosphatase; Repeat; Signal;	
KW	Transmembrane.	
FT	SIGNAL	1 28 Potential.
FT	CHAIN	29 1238 Protein-tyrosine phosphatase etc.
FT	DOMAIN	29 876 Extracellular (Potential).
FT	TRANSMEM	877 897 Potential.
FT	DOMAIN	898 1238 Cytoplasmic (Potential).
FT	DOMAIN	40 130 Fibronectin type-III 1.
FT	DOMAIN	170 266 Fibronectin type-III 2.
FT	DOMAIN	267 354 Fibronectin type-III 3.
FT	DOMAIN	356 440 Fibronectin type-III 4.
FT	DOMAIN	442 528 Fibronectin type-III 5.
FT	DOMAIN	529 618 Fibronectin type-III 6.
FT	DOMAIN	620 712 Fibronectin type-III 7.
FT	DOMAIN	717 803 Fibronectin type-III 8.
FT	DOMAIN	966 1238 Protein-tyrosine phosphatase.
FT	ACT_SITE	1140 1140 Phosphotyrosine intermediate (By similarity).
FT	CARBOHYD	62 62 N-linked (GlcNAc . .) (Potential).
FT	CARBOHYD	78 78 N-linked (GlcNAc . .) (Potential).
FT	CARBOHYD	85 85 N-linked (GlcNAc . .) (Potential).
FT	CARBOHYD	90 90 N-linked (GlcNAc . .) (Potential).

Query Match	64.1%	Score	4508.5	DB 1	Length	1238
Best Local Similarity	67.2%	Pred.	No. 4.7e-247			
Matches 901	Conservative	108	Mismatches	226	Indels	105
					Gaps	12

[illegible]

Db	382	KSPELFIKQDGEKGRNASTNGQVYWE DLKPGNSYHPEILPRGPDGTEGLASTVNGST	441
Qy	540	PSAVPDHHVYVTTTTEMLDMKSPDGASEYHYHLYVSKHGS-NHTSYIDAQLTQGLIP	598
Db	442	PSAATVDIRVNNI STTEMQLEWQNTDDASGYVYHVLSEKSGSII RTNNSOKMITVGSLLP	501
Qy	599	GLTNITITSPEVDHVMQDPNSTAQYTPSPNSVNSIDVSTNTAATLSMQNFPDASPTSYXC	658
Db	502	GLTNVITLFPFVDQIQGISNITQYTRPSSVSHLEVNTITTTAAIRMKNEEASASVAYS	561
Qy	659	LLIEKAGNSNATQVLT-DIGITATATYTELIPGSSYVEILPAQVGDGIKSLDEPKRSFCT	717
Db	562	VLIKTGSGSVNTSNFTQDPSI---LIPELIPGYSYTKILTYQGDGTTSLPQMLNLECT	618
Qy	718	DPASMASFDCVNPKEPALVILKMTQPCPGANNGFELEVSSGAMNNATHLESCSSENGETBYR	777
Db	619	EPEPITSFHCCEVNPKEPALVILKMACPFQMYGFELGVRSDMDMNTIRLENCTSDDDTECR	678
Qy	778	TEVYITNSTSYNISITTVSGCKMAAPRNKCTTGINDP RPDPSPNTTSVSHSVKPF	837
Db	679	TEVYITNSTSYNISITATLSCGKMAAPRNKCTTGINDP RPDPSPNTTSVSHSVKPF	738
Qy	838	SGFEASHGPIKAYVAVIILTTGAGHPASADVLKYYTDDFKGASDPTVYTLIRTEKGRSQS	897
Db	739	SGFEASHGPIKAYVAVIILTTGAAHPASADVLKYYTDFPRGASDPTVYTLIRTEKGRSQS	798
Qy	898	LSEVLKTEIDVNGESTTLGYNNGKLEPLGSRVACVAGFTNITFHPQNKGLIDGAEYSVF	957
Db	799	LSEVLNTEIDVNGESTTLGYNNGRLEPLGSRVACVAGFTNITVNIQNGLINGDESYSVF	858
Qy	958	SRYSNAGVSLPDPRGVICGAVFGCIPGALVITYNGGFI FWRKKRDANKNEVSFQIKPKK	1017
Db	859	SPYSBAVFLPDPRGVICGAVFGCIPGALATVAVGGFI FWRKKRDANKNEVSFQIKPKK	918
Qy	1018	SKLIRVENFEAYFPKKQADNSCGFAEEYEDLKLVGISOPKAAELAEENRGNRYNNVLPY	1077
Db	919	SKLIRVENFEAYFPKKQADNSCGFAEEYEDLKLIGISLPKTALEAENRGNRYNNVLPY	978
Qy	1078	DISRYKLSVQTHSTDYDINANNYMGYHSKODFIATQGLPNTLKD FWRMWEKUNYALIM	1137
Db	979	DISRYKLSVQTHSTDYDINANNYMGYHSKODFIATQGLPNTLKD FWRMWEKUNYALIM	1038
Qy	1138	LTKCYEQGRTCEBEYSPSKQADYGDITVANTSEILPEMTIRDPYKNITQTSBHPKQ	1197
Db	1039	LTKCYEQGRTCEBEYSPSKQADYGDITVAMTSEVLPEMTIRDPYKNITQTSBHPKQ	1098
Qy	1198	FHFPSMPGHGVPDPTDLLINFRYLVRODMKSPESPFLVHCSAGVGRTGFIAIDRLIY	1257
Db	1099	FHFPSMPGHGVPDPTDLLINFRYLRDPMKQIPESPFLVHCSAGVGRTGFIAIDRLIY	1158
Qy	1258	QIENENTVADVGIYVDLHRHPLMWQTEDDQVFLVNOCTVLDIVRSQKSKVDLIYQNTTAM	1317
Db	1159	QIENENTVADVGIYVDLHRHPLMWQTEDDQVFLVNOCTVLDIIRAQKSKVDLIYQNTTAM	1218
Qy	1318	TIYENLADVTTPGKTNGYIA 1337	
Db	1219	TIYENLEPVSWMFGKTNGYIA 1238	
RESULT 4			
062884			
ID	Q62884	PRELIMINARY:	PRT, 1216 AA.
AC	Q62884:		
DT	01-NOV-1996	(Tremblrel. 01. Created)	
DT	01-NOV-1996	(Tremblrel. 01. Last sequence update)	
DT	01-MAR-2004	(Tremblrel. 26. Last annotation update)	
DE	Density-enhanced phosphatase-1 precursor (EC 3.1.3.48) (Dep-1)		
DE	(Vascular protein tyrosine phosphatase 1).		
OS	Name=Dep1;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		

Db 595 CMEPAQVDSLHCCEVVPKPEPALVLLKMACPCPGNNGSFEIGVRSDADAMNTHLENTLJDNDTE 654
Qy 776 YRREVTYTLNPNSTSVNISTTVSCGKMAAPNTNCTGTGTDPDPDGSNITSVSHNYSKV 835
Db 655 CREEVYTLNPNSTSVNISTATLSGKMMALPTOSTCTGTGTDPDPDGSNITSVSHNYSKV 714
Qy 836 KFSGFSEASHGPRIKAYAVLLTGEAGHPADVLKATYDDPFKAGADTYTYTLIRTEBKGRS 895
Db 715 KFSGFSEASHGPRIKAYAVLLTGEAGHPADVLKATYDDPFKAGADTYTYTLIRTEBKGRS 774
Qy 896 QSLSEVLKYEIDVNESTTLGYNGKLEPLGSYRACVAGFTNITFHONKGLIDGASBYV 955
Db 775 QGISEALNTEIDVNGOSTTLGYNGRLEPLGSYRACVAGFTNITFYNQNDLIDGDSBYV 834
Qy 956 SFSKYSNDAVSLPDPBGVYCGAVFCIRGALVYVVGFTFPRKKRKAANKNEVSFSQIKP 1015
Db 835 SFSKYSNDAVSLPDPBGVYCGAVFCIRGALVYVVGFTFPRKKRKAANKNEVSFSQIKP 894
Qy 1016 KKSGLIRVNEPEAFKQADNSCGFAEYEDLKLVGISOPEKVAELAENKGRYNNVL 1075
Db 895 KKSGLIRVNEPEAFKQADNSCGFAEYEDLKLVGISOPEKVAELAENKGRYNNVL 954
Qy 1076 PYDISRYKLSVQTHSTDDYINANYPGYHKKDFIATQGPLPNTLKDFWEMWMEKNYVYI 1135
Db 955 PYDISRYKLSVQTHSTDDYINANYPGYHKKDFIATQGPLPNTLKDFWEMWMEKNYVYI 1014
Qy 1136 IMLTCKYEQGRTKEEYWPSPQADYGDITYAMTSEIYLPBWTIRDFVKNQIOTSEHPL 1195
Db 1015 VMLTKCYEQGRTKEEYWPSPQADYGDITYAMTSEIYLPBWTIRDFVKNQIOTSEHPL 1074
Qy 1196 RQFHTSPMDHGVDPDTDLINFRYLVADYMKSPSPSPILVHGSAGVGTGTFLADRL 1255
Db 1075 RQFHTSPMDHGVDPDTDLINFRYLVADYMKSPSPSPILVHGSAGVGTGTFLADRL 1134
Qy 1256 IYQIENENTVDYVGIYVLDLRMRPLMVQTEQYVFLNCVLDIVRSQKSKYDILYQNTT 1315
Db 1135 IYQIENENTVDYVGIYVLDLRMRPLMVQTEQYVFLNCVLDIVRSQKSKYDILYQNTT 1194
Qy 1316 AMTIYENLAPYTTGKTNGYTA 1337
Db 1195 AMTIYENLAPYTTGKTNGYTA 1216

RESULT 5
08C1W9 PRELIMINARY; PRT; 1238 AA.
AC 08C1W9;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Protein tyrosine phosphatase receptor-like protein J.
GN Name=Ptpj;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvS1;
RX MEDLINE=22084386; PubMed=12089527; DOI=10.1038/ng903;
RA van Mezel T., Ruttenkamp C.A.L., Zanon C., Straasen A.P.M., Vlcek C.,
Celisoe T., Tripodis N., Groot P.C., Dauwerse H., van Ommen G.J.B.,
Demant P.,
"Ptpj is a candidate for the mouse colon-cancer susceptibility locus
Rt1 and is frequently deleted in human cancers."
RL Nat. Genet. 31:295-300(2002).
DR EMBL: AY038877; AAN11409.1;
DR EMBL: AY038861; AAN11409.1; JOINED.
DR HSSP: P18052; 1YFO.
DR MGD: MGI:104574; Ptpj.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.

DR GO: GO:0007507; P:heart development; IMP.
DR GO: GO:0001570; P:vasculogenesis; IMP.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN III-like.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; fn3; 6.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PTPPHPTASE.
DR SMART: SM00060; FN3; 7.
DR SMART: SM00194; PTPC; 1.
DR PROSITE: PS00853; FN3; 5.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PP; 1.
KW Hydrolyase; Receptor.
SQ SEQUENCE 1238 AA; 136712 MW; DC294E254395B6C CRC64;
Query Match 63.8%; Score 4483.5; DB 2; Length 1238;
Best Local Similarity 66.9%; Pred. No. 1.2e-245;
Matches 897; Conservative 109; Mismatches 229; Indels 105; Gaps 12;
Qy 1 MKPAPARLPPSPGRLMALPLLLLRGLIACGTSPIPDPSVATVATGENGITQ 60
Db 1 MKPAPARLPPSPGRLMALPLLLLRGLIACGTSPIPDPSVATVATGENGITQ 43
Qy 61 ISSFASFFHQNGTQVETNNTSEDESSGANDSLTPPEGSGNGTDGASQKTPSSTGPS 120
Db 44 ----- 43
Qy 121 PVFDKAVSISPTNVILTWKSNPTDPAEYKVVYHKKNEKTIIVHQPCNITGLRPA 180
Db 44 --FDIEAV-VSPISVLLTWKHNSGASECR--IENKRESNLTFPVKQTSNITGLSPGT 98
Qy 181 SYVFSITPFGIGNETGDPRIYKVTPEIPVSDLRVALTYRKALSSNGNGTSCRYLL 240
Db 99 SYTFSIISVTNTEMLNK---TITTEPMVPSDLHTVSVGLYQALTWKSNAGTASYMLI 154
Qy 241 ESIGSHEBLQDSSLQVNIISDLKPGVOYNINPYLL--QSNKTKGDPGLGTEGGLDASNTERS 299
Db 155 EELTTHS-----SVNISGLKPGTN--NSFAPPSNETOADPAVAEVPDANGTKRI 203
Qy 300 RAGSPFAPVHDESLVGPVDSGQGSQSDTEVLTGLGEPGRTYNAVYVSOANGTEGQPOA 359
Db 204 PV-TNLSQLKHNKSVS-VDPSPGQDPSLTETLTLDLKPDQYNAVITYSOANGTEGQPRN 261
Qy 360 IEFRTNALIYQFDTYNAVISATSLTLTKVSDNESSNYTKIYHAGETSSNLNVSEBRA 419
Db 262 KVFETNSTQVSDVYANMISASMTLTKVSNVDSGRTSIYVKIYHAGGTHSVNQTVNKTEA 321
Qy 420 VTPGLASTFTYNTVTCVLDIGTSGFLQVHPVPVSDPRVYVSTTEIGLAWSSHDA 479
Db 322 IILGLSSSTLYNTVHPFLQGTBGPFLQVYISPDQVSDPRVYVSTTEIGLAWSSHDS 381
Qy 480 ESPQMIHTQEGAGNSRVEITTNOSIIGGLFPGTKYCFEIVPKPNTTEGASRTVNCRTV 539
Db 382 KSEFIRFKQDGEGRHASTNGOSYMWEDLKPGSYHFEIILPRPDGTGEGISVNVSTD 441
Qy 540 PSAVFDIHVVYVTTTMLDMKSPDGASEYVYHLVIESKGS-NHTSYDKAITLQGLIP 598
Db 442 PSAVTDIRVVNISTEMQLEQNQNTDASGYVHLVLESKGSIRRTSSQKMITVGSLLP 501
Qy 599 GTLVNITISPRVHVMDPSTAGTAPSVNVDVSTNTTAATLSQNPDPDASPTSYSC 658
Db 502 GTLVNITIPREVDDIIGISNITQYTRPSSSHLEVNTTTTAIRKMGEDPAASASTAYS 561
Qy 659 LLIKAGNSNATQVVT-DIGITDATVTEILPGSSVYVEIFAQYGDGKISLEPRKSFCT 717
Db 562 VLIKTGDSGNVSNFHKPSI---LIPELIPGVSIVYKILTYQGDGTTSLVPMNLECT 618
Qy 718 DPASMASPDCEVVPKPEPALVLLKMACPCPGMYTGFEIGVRSDSWDMTRLENCTSDDECR 777
Db 619 EPBVTSTFHCCEVVPKPEPALVLLKMACPCPGMYTGFEIGVRSDSWDMTRLENCTSDDECR 678


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QY 778 TEVTYLNFSSTSYNISTITVSCGMAAPTNTCTGTIDPPPPGSPNITSVSHNSVKYK 837
DB 679 TEVAVLNFSSTSYNISTITVSCGMAAPTNTCTGTIDPPPPGSPNITSVSHNSVKYK 738
QY 838 SGFEASHGPIKAYAVILITTEGAHPSADVLKTYDDFKKASDITYVYLLIRTEEKGSGS 897
DB 739 SGFEASHGPIKAYAVILITTEGAHPSADVLKTYDDFKKASDITYVYLLIRTEEKGSGS 798
QY 898 LSEVLKYEIDVGNESSTLTGYNKGLEPIGYSRACVAGFNITFHQNGLLDNGASSYVF 957
DB 799 LSEVLNVEIDVGNOSTLTGTNGRLEPIGYSRACVAGFNITFYNQNDGLNGDSSYVF 858
QY 958 SKYSDAVSLPDDPGVTCGAVFGCIGALVITVGGFIEMRKRRKAKANNVSSFSQIKPKK 1017
DB 859 SPYSEAVFLPDDPGVTCGAVFGCIGALVITVGGFIEMRKRRKAKANNVSSFSQIKPKK 918
QY 1018 SKLIVENVEAFKQKQADNSNGCFABEYEDLKVGISQPKTAAELAEENRGNRYNNVLPY 1077
DB 919 SKLIVENVEAFKQKQADNSNGCFABEYEDLKVGISQPKTAAELAEENRGNRYNNVLPY 978
QY 1078 DISRYVLVSQTHSTDDYINANYPGHSKQDPIATQGPLPNTLKDPMFMWMEKXNYATIM 1137
DB 979 DISRYKLVSQTHSTDDYINANYPGHSKQDPIATQGPLPNTLKDPMFMWMEKXNYATIM 1038
QY 1138 LTKCVQGGRTKCEEYWPSSKQADYDITVAMTSEIVLPEMTIRDPYVNIQTSSEHPLRQ 1197
DB 1039 LTKCVQGGRTKCEEYWPSSKQADYDITVAMTSEIVLPEMTIRDPYVNIQTSSEHPLRQ 1098
QY 1198 FHFSTWPHQVDDTDLINFRYLVRDWMKQSPSSPILVHCSAGVGTGPIADRLIY 1257
DB 1099 FHFSTWPHQVDDTDLINFRYLVRDWMKQSPSSPILVHCSAGVGTGPIADRLIY 1158
QY 1258 QIENENTVDVYGIYVDLEHMRPLMVTEDQYVFLNQCVLDIYRSQKSDKVLIIYONTAM 1317
DB 1159 QIENENTVDVYGIYVDLEHMRPLMVTEDQYVFLNQCVLDIYRSQKSDKVLIIYONTAM 1218
QY 1318 TIYENLAPVTTFGKTNGYIA 1337
DB 1219 TIYENLAPVTTFGKTNGYIA 1238

RESULT 6
Q6P4H4 PRELIMINARY; PRT; 539 AA.
AC Q6P4H4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE PTPRJ protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Ditchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carrincci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

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RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Klausner R.;
RA Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063417; AA063417.1; -.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; fn3; 4.
DR PROSITE; PS00853; FN3; 3.
SQ SEQUENCE 539 AA; 57189 MW; E970DA55A6B2E38D CRC64;

Query Match 39.6%; Score 2784; DB 2; Length 539;
Best Local Similarity 99.8%; Pred. No. 1,1e-149;
Matches 537; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKPARBARLPSPSPGRLMALPLILLRLGQILCAGTSPPIPDSPVATVATGNGITQ 60
DB 1 MKPARBARLPSPSPGRLMALPLILLRLGQILCAGTSPPIPDSPVATVATGNGITQ 60
QY 61 ISSFAEFHONGGTQOVETNTSEDESSGANDSLRTPGSGNGTGAGSOKTSSSTGPS 120
DB 61 ISSFAEFHONGGTQOVETNTSEDESSGANDSLRTPGSGNGTGAGSOKTSSSTGPS 120
QY 121 PVFDIKAVSISPTNVLITWKSNDTPAASEYKYVYHKMENEKITTIVHQPCNITGLRPA 180
DB 121 PVFDIKAVSISPTNVLITWKSNDTPAASEYKYVYHKMENEKITTIVHQPCNITGLRPA 180
QY 121 PVFDIKAVSISPTNVLITWKSNDTPAASEYKYVYHKMENEKITTIVHQPCNITGLRPA 180
DB 121 PVFDIKAVSISPTNVLITWKSNDTPAASEYKYVYHKMENEKITTIVHQPCNITGLRPA 180
QY 181 SYVSTIPGIGNETWGPRIYKTYTTEPIPVSDIRVALTGKRAKALSMNSNGTASCVL 240
DB 181 SYVSTIPGIGNETWGPRIYKTYTTEPIPVSDIRVALTGKRAKALSMNSNGTASCVL 240
QY 241 ESIGSHELTQDSRLQVNIIDLKRGVQYINPVLQSNKTKGDPPLGEGGLDASNTESR 300
DB 241 ESIGSHELTQDSRLQVNIIDLKRGVQYINPVLQSNKTKGDPPLGEGGLDASNTESR 300
QY 301 AGSPFAPVHDESLVGPVDPSSGOQSDTEVLVLGEBGTGYNATVVSQAANGTEGPOAI 360
DB 301 AGSPFAPVHDESLVGPVDPSSGOQSDTEVLVLGEBGTGYNATVVSQAANGTEGPOAI 360
QY 361 BFRNALQVDPDAVNVISATSLTIWKVSDNESSNTYKIHVAGETDSSNLVSEPRAY 420
DB 361 BFRNALQVDPDAVNVISATSLTIWKVSDNESSNTYKIHVAGETDSSNLVSEPRAY 420
QY 421 IPGLRSTFYNIITVCPVLGDIEGTPEFLQVHTPPVPSDFRVTVVSTTEIGLAWSSHDAE 480
DB 421 IPGLRSTFYNIITVCPVLGDIEGTPEFLQVHTPPVPSDFRVTVVSTTEIGLAWSSHDAE 480
QY 481 SFQWHTIQEGAGNSRVEITTNOSIITIGLFPGRKYCEIYVKPKNGTGASRTVCNRT 538
DB 481 SFQWHTIQEGAGNSRVEITTNOSIITIGLFPGRKYCEIYVKPKNGTGASRTVCNRT 538

RESULT 7
Q9W6V5 PRELIMINARY; PRT; 1406 AA.
AC Q9W6V5;
ID Q9W6V5;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Supporting-cell antigen precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=92296852; PubMed=10366616;
RA Kruger R.P., Goodyear R.J., Legan P.K., Marchol M., Raphael Y.,
R Cotanche D.A., Richardson G.P.;
RT "The supporting-cell antigen: a receptor-like protein tyrosine
phosphatase expressed in the sensory epithelia of the inner ear.";
RL J. Neurosci. 19;4815-4827(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RA Legan P.K.;
RX Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ238216; CAB41885.2; -.
DR HSP: P18052; IYFO.
DR GO: GO:0016787; P:hydrolase activity; IEA.
DR GO: GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN III-like.
DR InterPro: IPR000387; TYR phosphatase.
DR InterPro: IPR000242; Tyr_Ep.
DR Pfam: PF00041; FN3; 8.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PRO0700; PRTPPHPTASE.
DR SMART: SM00060; FN3; 9.
DR SMART: SM00194; PTPc; 9.
DR PROSITE: PS50853; FN3; 9.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS00383; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
DR HydroLase: Signal.
FT SIGNAL 1 24 Potential.
SQ SEQUENCE 1406 AA; 154213 MW; 2D609885CC0F367B CRC64;
Query Match 39.2%; Score 2752.5; DB 2; Length 1406;
Best Local Similarity 45.7%; Pred. No. 2.9e-147;
Matches 624; Conservative 169; Mismatches 459; Indels 112; Gaps 35;

Db 545 MVND-----TASDSTYRIEVRNGSVNNKTSNIPEITGLNGLCTLYTTFVAVA 596
Qy 525 NG-TEGASRTVCRTVSAVEDIHVVYVTTTMMWLDKSPD-GASEYVHLVIESKAGS- 581
Db 597 DGETEGGASISVYTKRAVLAHLKTEVGVTSVNLVTWVNDTSASTYR--IEVRNGSS 654
Qy 582 --NHTSTYDKAIIQGLIPGLTYNITISPEV--DHVGDNSSTAQYTPRSVNSIDVSTN 637
Db 655 INNKTSDITDA-EITGDPGLTYFTVFVAADQGTAGEGASISLYTKPSVNLKAEVY 713
Qy 638 T-TAATISWQNPDDASTYSCYLIEKAGNS-SNAQVVDIGITDAVTELLPGSSYV 695
Db 714 TMTSVNLTMVWNAESASYTY--RIEVAHSLINETW----SNVTKSIYVLLIPGISYNF 767
Qy 696 EIPAVQDGIKSLPGRKSCPTDPASWASPCDEVVPEPALVLRKTPCGNAGFELEVS 755
Db 768 TTFPAADNQTGEGGASISQNTYPPSSNAQCEAVNAMSITLTKMPCPYGGYSFDIEIF 827
Qy 756 SGAMNNATHESSCSSENGTE-YRTEVYVLPSTSYNISITTVSCGKMAAPTRNTCTTGIT 814
Db 828 NGTWTKKQSQFCGRSESEIFKTEP--LDYKYTYVSVTVSDGLTSLPVQKICTKSIT 885
Qy 815 DPPPDGSPNITSYSHNSVYKKSGFASHGPIKAYV-ILTTGAGHPADVLKTYDD 873
Db 886 DPVFNKAPLVKAVSHNSLSVEFPDFESVNGPLKAYVAMVTEAEGCLPSKSDLDITYND 945
Qy 874 FKGAADTYVYVIRTEKRSOSLSEVLKYEIDVNGESTLIGYNGKLEPLGSRACVA 933
Db 946 FKQMTATVYVYVLDVEIG--SSHSQNGNIYDVGGNTMYGGENPLPLHSYRASVA 1004
Qy 934 GFTNITFHPONKGLIDGASVYSPRSYSDAVSLPQDPGVI CGAVFGCI FGALVIVTVGGF 993
Db 1005 GFTNINTVANK--IMEQSYVSFSPCEVSVSLPQDPGVLAGAVIGCLAILAVVALIGY 1062
Qy 994 IFWRKKKADONNEVSSQIKPKSKLIRYENFAFYKKQADNSCGFAEYEDLKVGI 1053
Db 1063 IFWRRRKDKRNTNEVSPIKIKKSKMIKYENFESYKQADNSCGFAEYEDLKAGV 1122
Qy 1054 SOPKYAEIAENGNKNNVNLPPDISRVKLSVQTHSTDDYINANNVPGYHKKDFIATQ 1113
Db 1123 HQPKFAELIENKKNVNLPPDISRVKLSNPSCTTDDIINNANVPGYSSKAFILAAQ 1182
Qy 1114 GPLPNTLKDFWRMWEKNVYAIIMLTKEVCGRTKCEBYMPSKQADYGDITVAMTSEIV 1173
Db 1183 GPLPNTIEDFWRMWEKNISYVWLTKCEQARTKCGQYMPDQSKSYGDIIVMVEEV 1242
Qy 1174 LPEWTIRDFYKNIQISESHPLRFHFTSWPDHGPEDTDLINFRYLVRDYMKQSPES 1233
Db 1243 LPEWTIRDFVVENADTWEHSTVQFHTSWPDHGPEDTDLINFRHLVHEYSQNPIDS 1302
Qy 1234 PIIVHCSAGVGRCTFPAIDRLTYQIENENTVDYVGLRMRPLMVGOTEDQYFLNQ 1293
Db 1303 PIIHCSAGVGRCTFPAIDRLTYQIENENTVDYVGVYDLRMRPLMVGOTEDQYFLNQ 1362
Qy 1294 CVLIDIVRSQDSKVDLIYQNTAMTIYENLAPVTFPGKTYGIA 1337
Db 1363 CVMIDIRSQKCKTDLTYQNTAMAIYENFTPGAFPKANGYHA 1406

RESULT 8
Q9NPRS PRELIMINARY; PRT; 425 AA.
AC Q9NPRS;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PTRR, protein tyrosine phosphatase receptor J, eta (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Aulfray C., Amorge W., Ballabio A., Estvill X., Gibson K.,
 RA Lehrach H., Poustka A., Lundeberg J.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Andreu N., Estvill X., Escarceller M., Sumoy L.,
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ359057; CAB94390.1; -
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN_III-like.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS00853; FN3; 1.
 DR Receptor.
 FT NON TER 425 425
 SQ SEQUENCE 425 AA; 45078 MW; BD1ACA5D345B7027 CRC64;
 Query Match 31.1%; Score 2184; DB 2; Length 425;
 Best Local Similarity 99.8%; Pred. No. 8.7e-116;
 Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKPAREARLPSPSPGLRWALPILLILLAGQILCAGGPPSPIDPSVATVATGNGITQ 60
 DB 1 MKPAREARLPSPSPGLRWALPILLILLAGQILCAGGPPSPIDPSVATVATGNGITQ 60
 QY 61 ISSVASFHKQNGTGTPOVEINTSEDESSGANDSLRPEQSGNGTDGASOKTPSSTGPS 120
 DB 61 ISSVASFHKQNGTGTPOVEINTSEDESSGANDSLRPEQSGNGTDGASOKTPSSTGPS 120
 QY 121 PVFDDKAVSISPTNYILTMKSNDTASEKYYVYKHKMENEKITYVHQPCNITGLRAT 180
 DB 121 PVFDDKAVSISPTNYILTMKSNDTASEKYYVYKHKMENEKITYVHQPCNITGLRAT 180
 QY 181 SYVFSITPGIGNETWGDPRVIVITEPIPVSDLRVALTGVRKAAALSMNGNGTASCRVL 240
 DB 181 SYVFSITPGIGNETWGDPRVIVITEPIPVSDLRVALTGVRKAAALSMNGNGTASCRVL 240
 QY 241 BSIGSHEHETDLSRIQVNIISGLKPGVQVYNINPYLLQSNKTKGDPGTEGIDASTESR 300
 DB 241 BSIGSHEHETDLSRIQVNIISGLKPGVQVYNINPYLLQSNKTKGDPGTEGIDASTESR 300
 QY 301 AGSPAPAPVDESLVFPVPSGQSRDTEVLLVGLPGTRYNATVYSGAANGTSGQPAI 360
 DB 301 AGSPAPAPVDESLVFPVPSGQSRDTEVLLVGLPGTRYNATVYSGAANGTSGQPAI 360
 QY 361 EFRINAIOVFDVTAVNISATSLTLLIMKVSNDNESSNTYKLIHAGETDSSMLANTSEPRAY 420
 DB 361 EFRINAIOVFDVTAVNISATSLTLLIMKVSNDNESSNTYKLIHAGETDSSMLANTSEPRAY 420
 QY 421 IPRGLR 425
 DB 421 IPRGLR 425
 RESULT 9
 Q61373 PRELIMINARY; PRT; 361 AA.
 ID Q61373
 AC Q61373
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Protein tyrosine phosphatase (Fragment).
 GN Name=Prtp; Synonyms=Prp-RI9;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57/BL6; TISSUE=Liver;
 RA Higashitsuji H., Arai S., Furutani M., Imamura M., Kaneko Y.,
 RA Takenawa J., Nakayama H., Fujita J.;

RT "Enhanced expression of multiple protein tyrosine phosphatases in the
 RT regenerating mouse liver: Isolation of Prp-RL 10, a novel
 RT cytoplasmic type phosphatase with sequence homology to cytoskeletal
 RT protein 4.1." (1995).
 RL Oncogene 0:0-0(1995).
 DR EMBL: D49393; BAA08386.1; -.
 DR HSSP: P18052; IYPO.
 DR MGD: MGI:104574; Prtpj.
 DR GO: GO:0005615; C:intracellular space; TAS.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0007507; P:heart development; IMP.
 DR GO: GO:001570; P:vascularogenesis; IMP.
 DR InterPro: IPR00387; TYR phosphatase.
 DR InterPro: IPR00242; TYR PP.
 DR Pfam: PF0102; Y phosphatase; 1.
 DR PRINTS: PR00700; PRTPPHRTASE.
 DR SMART: SM00194; PTP; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS50055; TYR_PHOSPHATASE_PP; 1.
 DR Hydrolase.
 FT NON TER 1 1
 SQ SEQUENCE 361 AA; 41726 MW; B51462B8D11023AA CRC64;
 Query Match 26.3%; Score 1847; DB 2; Length 361;
 Best Local Similarity 94.7%; Pred. No. 9.2e-97;
 Matches 342; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 977 VFGGIFRALYIVYVGGIFFRKKRKDAKNNVSPSQIKPKSKLIRVENFEAFKKQAD 1036
 DB 1 VFGGIFRALYIVYVGGIFFRKKRKDAKNNVSPSQIKPKSKLIRVENFEAFKKQAD 60
 QY 1037 SNGCFAEYEDLKLVGISQPKYAAELAKNRKRYNNVLYDLSRYKLSVQSTSDYIN 1096
 DB 61 SNGCFAEYEDLKLIGISLEKTAELAKNRKRYNNVLYDLSRYKLSVQSTSDYIN 120
 QY 1097 ANTPMGHSKKDITATDGPLNTLKDFWRVWKEKNVYAILMTKCYEQGRTKCEYWPSS 1156
 DB 121 ANTPMGHSKKDITATDGPLNTLKDFWRVWKEKNVYAILMTKCYEQGRTKCEYWPSS 180
 QY 1157 QAQDYGDIYAMTSEIVLPMTIRDTYVKNIQSESHPRQPHFTSWPHGVPTDILLI 1216
 DB 181 QAQDYGDIYAMTSEIVLPMTIRDTYVKNIQSESHPRQPHFTSWPHGVPTDILLI 240
 QY 1217 NFRYLVDYKQSPSPSPILVHCSAGVGTGFIAIDRLIYOIENTVDDVGIYVDLDM 1276
 DB 241 NFRYLVDYKQSPSPSPILVHCSAGVGTGFIAIDRLIYOIENTVDDVGIYVDLDM 300
 QY 1277 HREPLMGTEDQYVFLNQCVDIVRSQDSKVDLIYONTTAMTIYENLAFTTGGKTNGYI 1336
 DB 301 HREPLMGTEDQYVFLNQCVDIVRSQDSKVDLIYONTTAMTIYENLAFTTGGKTNGYI 360
 QY 1337 A 1337
 DB 361 A 361
 RESULT 10
 Q8CIW2 PRELIMINARY; PRT; 1998 AA.
 ID Q8CIW2
 AC Q8CIW2
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 26, Last annotation update)
 DE Vascular endothelial protein tyrosine phosphatase.
 GN Name=Prtpb;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swiss Webster;

RX MEDLINE=22220060; PubMed=12234928; DOI=10.1093/emboj/cdf497;
 RA Navoroth R., Poell G., Ranft A., Kloeppel S., Samulowitz U., Fachinger G.,
 RA Golding M., Shima D.T., Deutsch U., Westwieser D.;
 RT "VE-PTP and VE-cadherin ectodomains interact to facilitate regulation
 RT of phosphorylation and cell contacts.";
 RL EMBO J. 21:4885-4895 (2002).
 DR EMBL; AY077755; AAL75813.1; -
 DR HSP; P18052; 1YPO.
 DR MGD; MGI:97809; Ptpb.
 DR GO; GO:0016787; F:Hydrolase activity; IEA.
 DR GO; GO:0004725; F:Protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:Protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003961; FN.II.
 DR InterPro; IPR008957; FN.III-like.
 DR InterPro; IPR000187; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00041; fn3; 15.
 DR Pfam; PF0102; Y_phosphatase; 1.
 DR PRINTS; PR0700; PRTYPHPTASE.
 DR SMART; SM00060; FN3; 16.
 DR SMART; SM00194; PTRC; 1.
 DR PROSITE; PS00853; FN3; 15.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
 DR Hydrolase.
 KW SEQUENCE 1998 AA; 224474 MW; B37EA6501EF03B5D CRC64;
 SO
 Query Match 17.9%; Score 1259.5; DB 2; Length 1998;
 Best Local Similarity 28.8%; Pred. No. 3e-62;
 Matches 378; Conservative 216; Mismatches 500; Indels 217; Gaps 45;

QY 104 NGTGAASQKTSSTGSPSPVPIKANSISTPTVILLTKNSNDPAASRYKVVHKKMENEKTI 163
 DB 805 SGQYEAASQGTGRITPEPVKDLTLNRSTEDLHVTWSPANEDVDQY--VQLLENDKVF 862
 QY 164 TVVHQPMCNITGLPATSYVF-SIRPG-----IGNETWGDPR--VIKITEPIPSDLR 214
 DB 863 PHIL-----VMTATKYFTALTGRHKYILVLTISGDVQASFIIGLVPSPVKNKH 915
 QY 215 VALTGVK-KAALSWNGNGTASCRVLLSISGHEELTQDSRLQVNI SLPKGVQVNIINPY 273
 DB 916 ISANGATRLMTWTSPPGG-----DVDSY 939
 QY 274 LLOSNKTKGDELGTBEGGLDASNTESRAGSPAPPHDSLYGVDPVSSGQGSRDTEVLV 333
 DB 940 VVSAFR-----ODEKVSQTIPIRQ-----ASEHTFH 965
 QY 334 GLPGRYRNATVYVSOANGTEGQPOAIEFRINAIOVPVTAVN-ISAATLTIWKVSDNE 392
 DB 966 RLEAGAKYRIATVS-VSGSLNQIDALG-QTVPAVQGVANAVSSSLVTSWOKALGV 1023
 QY 393 SSSNVTYKIHVAGETSSNLNVSEBRA-----VIFGLSSFTYNTVTCPEVLGDIETG 444
 DB 1024 AE---RYDILLNENGLLLSNVSEBAPARQKHFEELDTGSK---YKQOILTVSGGLRSK 1076
 QY 445 PCFLQVHTPPVPVSDFRITVSTTEIGLAWSHDSESQMI---TQGAAGSRPEI-TT 500
 DB 1077 ESQAEGRTVPAVNLRLITENSSRLSGMTASBGLSWYNIPLVNPDRITQERAAQVDP 1136
 QY 501 NQSLIIGLFGPTKTCFETVPRKPGTGAASRTVGNRTVPSAVFDIHVVYVYVTE-IMLD 559
 DB 1137 VQSFSGVQLLQGRYKMYIVH--SGELSNESFIRGRITVPAVNLKSHNTDLSLWFS 1194
 QY 560 WSPDGAEEYVHLVLESKGSNHTSTYDKAIT--LQGLIPG--TLVNTTISPVDHV 613
 DB 1195 WSPASGDDP-YELLVYNPNGTKENMKKEDVTEWRFGQLVGRKTYLVVYTHSGDLANK 1253
 QY 614 WGDPRSTQYTRPSVNSIDVSTNTATL---SMQFPDAS---PTYSYCLILEKAG 665
 DB 1254 VTGEGRTAP-SPPSLISPADVANVSLATVWGPDPMTVNPDELQWFGDALITFNYPSS 1312
 QY 666 NSSNATQVVTIDGIDATVTELLIPGSSYTVELIFAQVGDGIKSL-EPGRKSPCTDPASMAS 724

DB 1313 RKSEG-----RIVYGLHGRSYQSFVKTVSGDSWMTYKSPISGSVRYTPDKIQN 1361
 QY 725 PDCEVPEPEPALVUKTCPCPPANANGFELEVSSGAMNNAHLESSESGTEYRREVTYLN 784
 DB 1362 LHCR-PONSTAIACSWLPSPDSDPDGYSIE-----CRKDDTEIEFSRLKEKESILN 1412
 QY 785 F-----STSYNISITVYSCGMAAPTNTCTTGITDPPPDGSDNI-----TSVSHNSV 833
 DB 1413 IMLVPHKRYLVSLIKVGSAGTSEVEDSTITMIDRRPQP--PHIRNKEVDLISKSSI 1470
 QY 834 K-VKSGFEASHGPITAVAVILTTG-----EAGHPADVLKTYVDDEFKKASDRTYV 883
 DB 1471 NPTVNCWSFSDTNGAVKFAVAVREADSMDELKPEQGHPLPSYLEYRHNASIRVQTVY- 1529
 QY 884 TYLIRTEKGRSGLSEVLKKEIDVGNESITLG-----YNGKLEPIGSYRACVAG 934
 DB 1530 -FASKCAESPSSSKS-----FNILGAEMLSLGKCKDPGQKFDGPKPTAVRISIRA 1584
 QY 935 FTNITFPHQNGKLIDGABSVYFSRYSDAVSLPQDP--GVICGAVFGCIPGALVIVTVGG 992
 DB 1585 FTQLP-----DEDLKEFTKPLPSDTPPSPMTTESEPLFGVIEGYSAGLFLIGMLVALVAF 1640
 QY 993 FIFWRK--KRDADKNNEVSFSQIKP-----KSKSLRVENFEAYFKQQAQS 1037
 DB 1641 FICRQKASHRSRERSARLSIRDRPLSVHNLGQKGRKTCSPIKINGFEHFMKLQADS 1700
 QY 1038 NCGFAEVEDLKVIGISOPKFAELAEKGRNRNNVLPYDISVKLS-VQTHSTDQYIN 1096
 DB 1701 NYLLSKEVEDLKDQGRSQSCDIALPERGRNRRNNLIPYASVKLSNVDDPCSDYIN 1760
 QY 1097 ANYPGYHKKDPIATOGPLPNTLKDPEWRYWMEKNVYAIIMLTVCVEQRTKCEYMPSK 1156
 DB 1761 ASYIPGNFRREYIATGPELPBTGDDPRKAMQEQNHVAVTQCVBERGRKCHYVAD 1820
 QY 1157 Q-AADYGDITVAMTSEIVLPWTIRDTFTVKNIIQTSSEHPL-RQFHTSMPPHGVPTTDL 1214
 DB 1821 QDPLYYGDLILQWSESVLPFWTIRFEXICSEQDLAHLRIHFHYITVMPDHGVPELTQS 1880
 QY 1215 LINFRLVYDVMKQSPESPFLVHCSAGVGTGFIALDRILYQLENNTVYDVYGIYVDL 1274
 DB 1881 LIQFRTVRYDYINSPGAGPFWVHCSAGVGTGFVALLDRILQQLDSQSDVYIGAVHDL 1940
 QY 1275 RMHRPLWQTEQDQYVPLNQCLDIVRSQKSKVDLIYQNTAMTYENLAP 1325
 DB 1941 RLHRVHWQTECYVYHLCQVRYDLRAKGLRN---EQENLPLFIYENVP 1987

RESULT 11
 PTPB_HUMAN
 ID PTPB_HUMAN STANDARD; PRT; 1997 AA.
 AC P23467;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protein-tyrosine phosphatase beta precursor (EC 3.1.3.48) (R-PTP-beta)
 GN Name=PTPB; Synonyms=PTPB;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=9106018; PubMed=2170109;
 RA Krueger N.X., Streuli M., Saito H.;
 RT "Structural diversity and evolution of human receptor-like protein
 RT tyrosine phosphatases.";
 RL EMBO J. 9:3241-3252 (1990).
 CC -I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = proteicn
 CC tyrosine + phosphate.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

FT	CARBOHYD	574	574	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	598	598	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	652	652	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	721	721	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	829	829	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1040	1040	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1096	1096	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1163	1163	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1185	1185	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1212	1212	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1274	1274	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1367	1367	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1470	1470	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1474	1474	N-1linked	(G1CnAc . .)	(potential)	
FT	CARBOHYD	1518	1518	N-1linked	(G1CnAc . .)	(potential)	
SQ	SEQUENCE	1997	AA, 224267	MM, 691E99BA7A1515DD	CRC64,		
Query Match		17.7%	Score 1242;	DB 1;	Length 1997;		
Best Local Similarity		29.6%	Pred. No. 3e-61;				
Matches	397;	Conservative	190;	Mismatches	503;	Indels	251; Gaps
							53
QY	123	FDIAVASISPTNNVILTWKSDNTAASEYKVVYKHKHNEKITTVVHQPCNITGLRPATSY	182				
Db	759	FDHEVETIKNNKNNFOTKSIIP-----KSENE-----CVFVQVLPGRLY	796				
QY	183	VFSITPGIG-----NETWGDPRVIVKITEPIVPSDLRVALTGVRKAALSWNGNGRASCrv	238				
Db	797	SVATYTTKSGQYEANEO-GNGRTI-----PEEVKDLITNNRSTEDLHVTSANG-----	844				
QY	239	LLSEIGSHH-ELTQDSRL-----QVNISDLKPGVOY-----NINPYLQSNKT	280				
Db	845	---DVDQYEIQLLFNDMKVFPFPHLVMTATRYRFTSLRPGKQYKIVLVTISGDVQGSFI	901				
QY	281	KG-----DPLG-----TEGLDASN-----TERSRAGSTAPYHDESL	313				
Db	902	EGFTVPSAVKNIHISPGKATDLSLTVMTPGGGDVDSYTSAPRHSQKVDSTQIPRH-----	957				
QY	314	VGPVDPSSGQGSRDTEVLVLGLEPGRNATNAVYGOAANGTGPQOALFFRNALQVFDVT	373				
Db	958	-----VFHHTFHHLEAGDEQYQIMIAS--VSGSLKQNLNVGRIVPASCVI	1002				
QY	374	AVN-ISATSLTLTKVSDNESSNYTKIHVAGETSSNINLVSEPPA-----VIPGL	424				
Db	1003	ADNAYSSYSLIVSQAKAGVAA---RYDILLITENGILLNRTSPATTTKQKFEEDLTPGK	1059				
QY	425	RSSTFVNIIVCPVLGDIEGTFGFLQVTPRPVPSDFPVTVVSTTEIGLAWSHDAESRQM	484				
Db	1060	K-----YKIQILTVSGGLFSKEAQJEGRTVPAVLDLITENSTHLSRWRASGELSWY	1115				
QY	485	HI---TOEGAGNSRVEI-TTNQSIIGGLFPGTYCEIYKPGNGTEGASRTVCNRTVP	540				
Db	1116	NIFLNPDPGNLQERAQVDPVLQVSPSPONLLQGRMYKNVITW--SGELSNESFIFGRFP	1173				
QY	541	SAVEDIHVVVYTTTE-MWLDKMSPPDASBEVYHHLVIESKIGSNHTSYDAIT---LQGL	596				
Db	1174	ASVSHLGSNRNNTTDSLWFNWPSPASGPDF-YELLIVNPGTKKENKDKDOLTEWRFQGL	1232				
QY	597	IPGLTNNITISPEVDHWGDPNSTAQYTR-----PSNVSNIDVSTNTTAATL---SMON	647				
Db	1233	VPGKRYVLWV---VTHSGDLSNKTVALSRAPRSPSLMSFADIANITSLATITWKPDPMTD	1289				
QY	648	FDDASPTV---SYCLLIEKAGNSMATQVVTIDIGTATVTELIPIGSSYVEIYFAQVGDG	704				
Db	1290	YNFELQMLRDLALTYNPNYNNKRSBGRILYVG-----LRPGSYQFPNVKTVSGDS	1339				
QY	705	IKSL-EPGRKSFCTDPASMASPCEVAVPKEPALVLMKTCPRGANAGRELVSSAGMNNAT	763				
Db	1340	WKTYSKRPISBSYATTKPKIQNLHCR-PONSTALACSHIIPDSDFDGSIE-----CR	1390				
QY	764	HLSCSSENGTEYRTVEVYLVNF-----STSYNISITTVSCGNKAAAPRTNCTTGIDTPPP	818				
Db	1391	KMDTOEVEFRKLEKEKSLINIMWLVDHKKRYLIVISIKVQSGMTSEVEDSTITMIDRPP	1450				


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Db      1468 LPSYLEYRHNASIRVQTVY--FASKVENPNNSKSKS----FNILKGAEMESLGGKCDPT 1521
Qy      917 ---YYNGKLEPLGSAACVAGFNITFEHQNKGLIDGASVYSFSR--YSDA-VSLP--- 967
Db      1522 QQKFCDDPLKPHTAIRISTRALFO-----LFO--BDLKEFKPLVSDTFSLPTTT 1570
Qy      968 -ODPGVICAVFGCIGFALVI---VTVGGFIMWRKK--RKDAKNNEVSFSGIKP----- 1015
Db      1571 ESEF--LFGAIEGVSAGLFLIGMLVAVVALLICROKVSIGRRRPARSLIRDRPLSYHL 1628
Qy      1016 -----KSKLIRVENPEANFKQOADSNGFAEEYEDLKVIGISQPKYAAELAENRG 1067
Db      1629 NIGQKGNRTSCPIKNOFEHGMKLOADSNVILSKFEYELDVARNOSCDIALLPENRG 1688
Qy      1068 KRRYNNVLPYDISRYKLS-VQTHSTDDYINANVMGYSKSKDFIATOGFLPYTLKDFRM 1126
Db      1689 KRRYNNILPYDATRYKLSNVDDPCSDYINASYIFGNRRREYIVTQGLPETKDFWKM 1748
Qy      1127 VWEKNVYALIMLTKEVQGRITCEEWPSKQ-ADYGDITVAMTSEIYLPWTITRDTYK 1185
Db      1749 VWEQVNHVIMVTQCEKGRVACDRYMPADQDSLYYGDLILQMLSESVLPWTITREFKIC 1808
Qy      1186 NIGTESHPL-RQHFHTSWPDHGVPTDILLNFRLVVDYKQSPSPSPILVHCSAGVG 1244
Db      1809 GEEQDAHRLIRHFHYTPPDHGVPEPTQSLIQFVRYVADYINRSGAGPTVHCSAGVG 1868
Qy      1245 RTGFTIADRLIYQIENENTVDVGIYVYDLRMHREPLMOTEDQYVFLNQCVDLDIRSOKD 1304
Db      1869 RTGFTIADRLIYQIENENTVDVGIYVYDLRMHREPLMOTEDQYVFLNQCVDLDIRSOKD 1928
Qy      1305 SKVDLIYQNTTAMTYENIAP 1325
Db      1929 RS-----EQENPLFPIYENVNP 1945

RESULT 13
Qy      080VNT7 PRELIMINARY; PRT; 1102 AA.
AC      080VNT7;
DT      01-JUN-2003 (Tremblrel. 24, Created)
DT      01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT      01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE      Ptpb protein (Fragment).
GN      Name=Ptpb;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NMRI; TISSUE=Mammary tumor;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA      Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uscid T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Blakeley R.W., Touchman J.W., Green E.C., Shevchenko Y., Bouffard G.G.,
RA      Rodriguez A.C., Gilmour U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzyzanski M.I., Skalska U., Smalins D.B., Scherch A., Schein J.E.,
RA      Jones S.U., Warr M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NMRI; TISSUE=Mammary tumor;
RA      Strausberg R.;
RL      Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC047086; AAH47086.1; -.
DR      HSSP; P18052; IYFO.
DR      MGD; MGI:97809; Ptpb.
DR      GO; GO:0016787; F:Hydrolase activity; IEA.
DR      GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR      GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR      InterPro; IPR003961; FN III.
DR      InterPro; IPR008957; FN III-like.
DR      InterPro; IPR000387; TYR phosphatase.
DR      InterPro; IPR000242; TYR_PP.
DR      Pfam; PF00041; FN3; 6.
DR      Pfam; PF00102; Y_phosphatase; 1.
DR      PRINTS; PR00700; PTPYPPHPTASE.
DR      SMART; SM00060; FN3; 6.
DR      SMART; SM00194; PTPc; 1.
DR      PROSITE; PS00853; FN3; 6.
DR      PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR      PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR      PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW      Hydrolase.
FT      NON TER.
SQ      SEQUENCE 1 1 124677 MW; 8281DF729BP9148 CRC64;

Query Match 17.3%; Score 1219.5; DB 2; Length 1102;
Best Local Similarity 29.4%; Pred. No. 2.2e-60;
Matches 354; Conservative 197; Mismatches 455; Indels 199; Gaps 40;

Qy      201 IKVTEPIPVSDRLVALTGR-KAALSMNGNTASGRVLEISGHEBLTQSRQVNI 259
Db      6 IEGITVSTYKNIHISANGATDRIMVTSFGG----- 38
Qy      260 SLDKPGVQVNIINPYLLQSNKTKGDPLETEGLDASNTERSRAGSPAPVHDSLVGPVDP 319
Db      39 -----DVDSVVSAGR-----QEEKVDSQITPKG----- 62
Qy      320 SSGQGSRTVEVLVLGEPGRNATYVSGAANTBEGQPAQIERTTAIOVFYTVAN-IS 378
Db      63 -----ASEHTHRLIEAGAKRIATVS-VSGSLRNQIDALG-QTVPASQGVANAVS 113
Qy      379 ATSLTILMKVSDNESSNYTKIHVAGETDSNLVSEPPA-----VIRPLASTRY 430
Db      114 SNLTVTSMQALGVAE---RYDILLNENGLLSNVSEBARTARQHFEDLTGCK---Y 166
Qy      431 NITVCYVLGDIETGPGLQVHTPPVPSDFRVTVSTTEIGLAWSSHDAESFOMI--T 487
Db      167 KMQILTVSGGLFSKESQAEGRTPPAVTVMLRITENSSRYLSFGWTASBGLSMYNIFLYN 226
Qy      488 QEAGNSRVEI-ITNOSIIIGLFPQTKCFELVPGNGTSGASTVCNRTVPSAVPFI 546
Db      227 PDIITDERQAVDPVLVSFQNLQGRMYKMWIVTH--SGELSNESFIFGRTPPAVNH 284
Qy      547 HVVYVTTT-MMLDMKSPGASERYVHYLVTEKSGNHTSYDKAIT---LOGLFG--- 599
Db      285 KSGHRTTJSLWSWSPAGDPDF-YELLVNPNGKKNMKEKOVTEMRPGVLVGRKY 343
Qy      600 TLVNTITSEVDHVMGDNPSTQVTRPSNVSNIDVSTNTAATL---SWQNFDDAS--- 652
Db      344 TLVVVTHSDLSNKVYGBGRTPA-SPPSILSFADVANTSLAITWKGPDMTDYNDPQLW 402
Qy      653 -PVSYCLIEKAGNSNATQVVTIDIGTDAVTEILPSSYTVAFIAQVGGISL-EP 710
Db      403 FPDALTITNPVSRKSGE-----RIVYGLHPRSFSQSVKTVSGSWMTYSKXP 451
Qy      711 GRKSFTDPAVASPDCEVVPKEPALVLKTCPPGANAGFELEVSAGAMNATHLESSES 770
Db      452 ISGSVATKDKIQNLHCR-PQNSTALACSWIPPSDPFGYSIE-----CRKMDTQEI 502
Qy      771 ENGTERTREVTYLN-----STSYNISITTVSGCKMAAPTRNTCTTGITDPPPDGSPNI 825

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Db      503 EFSKLEKESKLINIMLVPHKRYLVSIKVGSAGTSEVEDSTITMDREPQC--DPHI 560
Qy      826 -----TSVHNSVK--VKPSGFASHGPIKAYAVILTTG-----EACHPADVLKY 869
Db      561 RVNEKDVLISSSINFTVNCSEWFSDTGAVYFVAVVAREADSMDELKEQOHPSPSYLEY 620
Qy      870 TYDDPFKASDPTVYTYLIRTEEKRSOSLSEVLKYEIDVNESTTLG-----YYNG 920
Db      621 RHNASIRVYQTN--FASKCAESPDSSSKS-----FNITLGEHMSLSGKCPDSQOKKCDG 674
Qy      921 KLEPLGSYRACVACFTNITTFHPQKGLDGAESYVSFSRYSDAVSLPDP--GVICGAVF 978
Db      675 PLKPHYATYRISIRAFQGF-----DEDLKEFTKPLYSDFPFMPITTESEPLFVGLGVSA 730
Qy      979 GCIFGALVITYVGFIFWKR--KKDKAKNEVVSQIKP-----KSKILRV 1023
Db      731 GLFLIGLVVAVFIFCRQKASHRSRPSARLSIRDRPLSVHLNLGQKGNKRTSCPIKI 790
Qy      1024 ENFEAYFKQOQADNSCGFAEYEDLKLVGISQPKYAEIAENRGKNRYNNVLPYDISRVK 1083
Db      791 NOFEGHFMKQADNSNLYLSKEYEDLKDVGSQSCDIALLPENRGKNRYNNILPYDASRVK 850
Qy      1084 L-SYQTHSTDDYINANMPGYSHSKDFIATQGPLNTLKDFFWVWEKXVYAIIMLTQCV 1142
Db      851 LCNVDDBPCSDYINASYIPGNPFREVIATQGPLPTGKDDFMKAMEQVANIWMVYQCV 910
Qy      1143 EOGRTKCEEYWPSCQ-AQDYDDITVANTSEIVLEWTRDTVKNITQSEHPL-RQHNF 1200
Db      911 EKGKVKCDHVPADQDPLLYGDLILQVWSESVLEBWTIREKILSEBGLDHRILRHPHY 970
Qy      1201 TSWPDHGVPTTDLINFRYLVRDYMKSPESPILVHSCAGVGTGFIAIDRLIYQIE 1260
Db      971 TWPDPHGVPTTGLIQFVRVRYDIINRSPAGFTVHCSAGVGTGFIALDILQGLD 1030
Qy      1261 NENTVDYGIYDLRMHRPLMVQTEDQYVFLNQCVLDIRVSQKSKVDLIYQNTAMTY 1320
Db      1031 SKDSVDYIGAVHDLRLRHVHVQTECYVLYHQCVRDYLAKKLRN-----EQENPLPFIY 1086
Qy      1321 ENLAP 1325
Db      1087 ENVNP 1091

RESULT 14
Q9HD43 PRELIMINARY; PRT; 1115 AA.
ID Q9HD43 AC Q9HD43;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Transmembrane-type protein cytosine phosphatase H.
GN Name=PTPRH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21328879; PubMed=11435690;
RA Marnett A.G., Mehenni H., Reichenberger E., Antonarakis S.E.,
RA Krieg T., Olsen B.R.;
RT "Gene for the human transmembrane-type protein cytosine phosphatase H
RT (PTPRH): genomic structure, fine-mapping and its exclusion as a
RT candidate for Peutz-Jeghers syndrome."
RL Cytogenet. Cell Genet. 92:213-216(2001).
DR EMBL: AF275130; AAF91411.1; JOINED.
DR EMBL: AF275132; AAF91411.1; JOINED.
DR EMBL: AF275133; AAF91411.1; JOINED.
DR EMBL: AF275134; AAF91411.1; JOINED.
DR EMBL: AF275135; AAF91411.1; JOINED.
DR EMBL: AF275136; AAF91411.1; JOINED.

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DR EMBL: AF275137; AAF91411.1; JOINED.
DR EMBL: AF275138; AAF91411.1; JOINED.
DR EMBL: AF275139; AAF91411.1; JOINED.
DR EMBL: AF275140; AAF91411.1; JOINED.
DR EMBL: AF275141; AAF91411.1; JOINED.
DR EMBL: AF275142; AAF91411.1; JOINED.
DR EMBL: AF275143; AAF91411.1; JOINED.
DR EMBL: AF275144; AAF91411.1; JOINED.
DR EMBL: AF275145; AAF91411.1; JOINED.
DR EMBL: AF275146; AAF91411.1; JOINED.
DR EMBL: AF275147; AAF91411.1; JOINED.
DR EMBL: AF275148; AAF91411.1; JOINED.
DR EMBL: AF275149; AAF91411.1; JOINED.
DR HSSP: P18052; 1YFO.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0016787; F: hydrolase activity; IEA.
DR GO: GO:0004725; F: protein tyrosine phosphatase activity; IEA.
DR GO: GO:0006470; P: protein amino acid dephosphorylation; IEA.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR008957; FN III-like.
DR InterPro: IPR000387; TYR phosphatase.
DR InterPro: IPR000242; TYR_PP.
DR Pfam: PF00041; FN3; 7.
DR Pfam: PF00102; Y_phosphatase; 1.
DR PRINTS: PR00700; PTPYPPHPTASE.
DR SMART: SMO0060; FN3; 7.
DR SMART: SMO0194; PTPc; 1.
DR PROSITE: PS50853; FN3; 7.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Transmembrane.
SQ
SEQUENCE 1115 AA; 122351 MW; A7A1AB24CFCD3846 CRC64;

Query Match 16.7%; Score 1176.5; DB 2; Length 1115;
Best Local Similarity 26.3%; Pred. No. 6.3e-58;
Matches 366; Conservative 188; Mismatches 456; Indels 383; Gaps 43;

8 ARLPSPRG-----LRMALPLLLLLRLRQGLICAGTSPPIPDPAVAT 53
25 ARAPAPNPNRNLYETOTTSISLSWEVP-----DGLDS--ONSRYWVCT 68
54 GENGITQISSTAESFHKQNGTGTPOVETNTSEDESSGA--NDSLRTPQCSNGTDAQ 111
69 GDGCTTETRTN-----TATNTVVDLGRGSLYTCVWKEKQVNSVGR-- 112
112 KTPSSTGSPVFDIKAVSISPTNVLITWKSNDTAASEYK-YVGHKMEKNEK--TITVHQ 168
113 -VTATAPNPNRNIRVBAQTSSIALTWVEVPDGPDPQNSTYGVETGDPGAGTRSTAH- 170
169 PWCNIT--GLRPAVSYSITPGIGNETWGDPRVIKVTBPIPVSDLRVALTGVRKALS 226
171 -TNTVTDGLEPGLVAFSMWVG-KNGINSRETRNATTANPNRNLEVEAQTTSSISLS 227
227 WSNNGTASGCVLLSISGSHBELTQDSRLQVNSDLKPGVQYNINPYLLQSNKTKGDLG 286
228 WEVPDGT-----PQNS-----TTCVQCT-----G 247
248 DGGRTETRTN-----PQNS-----TDTRTVVDGLGSGSLYTCGSVM 278
287 TEGGLDASNTERSRAGSPFAPVHDESLVGPVDPSSGQGRDTEVLVGLGEPRTNATVY 346
248 DGGRTETRTN-----PQNS-----TDTRTVVDGLGSGSLYTCGSVM 278
347 SQAANGTEGQPALEFRTNMQVFDYAVNISA---TSULTIMKVSNESSNTYKIHV 403
279 VE-----KGVNSVSEIYTSATAPNPNRNLYEATQNTSSIALTWVEVPDGPDPQNSTYGV 334
404 AGETSSNLINVSBRPAVIGLRSSTFYNTVCPIYAGDIBGTGFLQVH----- 451
335 TGDGGR-----GTRSTAHNTITVDRL-----EPGLLYFVSVWVGKGINSS 376
452 -----TPPVSDPFVTVVSTTEIGLAWSHDAE-----SFOHMTTQEGAGNSRVEIT 499
377 RETRNATTAPNPNRNLMETQNTSSIALCWEVDPGPYPODYTWVEYTGDG--GGTETRTN 435

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QY 500 TNGSIIGGLPFGTKYCFEIVPKPGNGTEGASRTVCNRTPVSAVPDHHVVTTEMD 559
DB 436 TMTSVTAERLEPGLTITFSVMAE-KNGAGSRONVSIITVPANVTSLSQDMNSTIAR 494
QY 560 WKSPPD--GASEVYHL--VIESHGSHNSTYDKAITLQGLIPGLYNTITISPEVDHWG 615
DB 495 WTAPQPGGSSYSYVWYSWREGMTDPRQTOSTGTDITLKELEAGSLYHLTWAEERVAG 554
QY 616 DPNSTAQYTRPSVNSINDVSTNTATLSMNF--DDASPTYSCLLIKAKN----- 666
DB 555 YNSTLTAAPRNVDTLONETQKSVLMWKAPGPHSQLYVYWQWASKGHPRGODP 614
QY 667 SSNAIOVVDIGITDATTTELIPGSSYVEIPAQVGDGKISLEPGKSPC--TDPASMAS 724
DB 615 QANWVNOTSRMTETWYKVALEBGLTYNFTWAERNDVASSTQ--SLCASTYDIYTI 670
QY 725 PDCEVVPKRPALVLMKTCPPGANNAGLELVSSGAMNATHLESCESENGETRYRTVYLN 784
DB 671 TSCVSTISAGYVNLWSPQGGYEAELELV-----GQORSGODRS----- 710
QY 785 FSTSVNISITTVSCGMAAPRTNTCTTGITDPPPDGSPNITSVSHNVKVFSGFEASH 844
DB 711 -----SCGEAVS-----VLGL----- 721
QY 845 GEIKAYAVILTTGEAGHSADVLKTYDDPKKASDTYVYLIIRTEKRGQSLSSEVLKY 904
DB 722 GARSTPATITTT-----IWDGK-----VYSH 743
QY 905 EIDVNGNESTTLGYNGKLEPLGSYRACVAGFNITFHPQNGKLDGASVYSFRYSNAV 964
DB 744 SYVCHTESA----- 752
QY 965 SLDPDPGYICGAVFCIGALVITVGGFIEMKKRKDKAKNNEVSFSQIKKSKL----- 1020
DB 753 -----GYIAGAFVGL--LELLVGLLIFLKKRNKK-----QKRELNDIVSS 796
QY 1021 ---IRVENPEAFKQADNSNGFAEEYEDLKVGISQPKAAELAKRGKRRNNVLPY 1077
DB 797 PGDIPAEFPADHVRKNERDSNGCFADKYQLSLVSHSQSOMVASSENNAKRYANVLPY 856
QY 1078 DISRVKLS-VQTHSTDDYINANMPGYSHKDFIATQGLPNTLKDFRWMWMEKNVYALI 1136
DB 857 DMSRVPLKPIHBEPSDYINASPMFGMLSPGFATQGLPQYTGDFRMLWEGQSHTV 916
QY 1137 MLTKVEGGRTKCEYWP-SKQADQDGYIYAMTSEIVLPFWTIRDFTVKNIQTSSEHL 1195
DB 917 MLTKCMGGRVCKCHYWP-LDSQPCPTHGLRYTLVGEEMENWTVRELLQLQVEBQKTL 976
QY 1196 RQFHTSPDHGVDPDITLLINFRYLVDYWKOSPPSPILVHGSAGVGTGFIATDRL 1255
DB 977 RQFHYQAMPDHGVSSPDTLLAFMRMRKQMLDQTMEGGPPIVHGSAGVGTGFIATDVL 1036
QY 1256 IYQIENENTVDYGIYVDLRMRPLMVTQEDQYVFLNQCVLDYR--SQKDSKVDLIYQN 1313
DB 1037 LROQSEBELQPFSEFVVRKMRRESRPLMVQTEAQYVFLHQCLIRFLQSAQAAPAEKVEYED 1096
QY 1314 TTAMTIYENLAPV 1326
DB 1097 VENL-IYENVAAT 1108

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RESULT 15

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ID 015426 PRELIMINARY; PRT; 1118 AA.
AC 015426;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Protein tyrosine phosphatase precursor.
GN Name=SAP-1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_taxid=9606;
RN
[1]
SEQUENCE FROM N.A.
RX MEDLINE=94124561; PubMed=8294459;
RA Macozaki T., Suzuki T., Uchida T., Inazawa J., Ariyama T., Matsuda K.,
RA Horita K., Noguchi H., Mizuno H., Sakamoto C., Kasuga M.;
RT "Molecular cloning of a human transmembrane-type protein tyrosine
phosphatase and its expression in gastrointestinal cancers.";
RL J. Biol. Chem. 269:2075-2081(1994).
DR EMBL; D15049; BA03645.1; -
DR PIR; A49724; A49724.
DR HSSP; P18052; 1YFO.
DR Genew; HGNC:9672; PPRH.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005001; C:transmembrane receptor protein tyrosine pho. .; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; FN3; 6.
DR Pfam; PF00102; Y_phosphatase; 1.
DR SMART; SM00060; FN3; 6.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS50853; FN3; 6.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR KEGG; K04005; Signal.
FT SIGNAL 1 25 potential.
FT CHAIN 26 1118 protein tyrosine phosphatase.
SQ SEQUENCE 1118 AA; 123038 MM; F73B3967ECES9F00 CRC64;

Query Match 16.1%; Score 1130; DB 2; Length 1118;
Best Local Similarity 25.9%; Pred. No. 2, 7e-55;
Matches 354; Conservative 181; Mismatches 453; Indels 380; Gaps 40;

QY 8 ARLPSPG-----LRALPLLLLRIGQILCAGCPSPIPPVSATVAT 53
DB 25 ARAPAPNGRNLVETQTTSSISLSWEV-----DGDS--QNSNWVQCT 68
QY 54 GENGITQISSIAESFKQNGKTGPQVETNTSDESSGA--NDSLRTPQSGNGTDGASQ 111
DB 69 GDGGETETENT-----TATVTVDGAGPSGLYCSVWEXDGVNSSVGT-- 112
QY 112 KPPSSGSPSPVDIKAVSISPTNVLLTWKSNPTASSEYK-YVYKAKMENK--TITVHQ 168
DB 113 -VTTATAPNPNKLRVLEAQNTSSIALTWEPDGPDPQNSTYGVVEYTGOGGAGTSTAH- 170
QY 169 PWCNIT--GLRPATSVFSITPGIGNETWGDPRVIVKITEPIPVSDLRVALTGVRKALS 226
DB 171 --TNITVDLEPGCIYAFSM----- 188
QY 227 WNGNGTASCRVLLESIGSHEELTQ---DSRLQVINIDLKRGVQYNINPYLQSNKTKG 282
DB 189 WVGKNGINSSRETNNATTAAHNVKRPESGSDHQHLEL- GGPFWH-RPTIELDLRTSA 246
QY 283 DPLTEGCLDAENSTRSRAGSPYAVHDESLVGPDPSPSGGQSRTEVLVLGLERGTYN 342
DB 247 LEMVAEGRLTEQTPES-----PVD-----GLRGSLEYT 275
QY 343 ATVYSQANGTEGQPAIEFRTNALQVFDYAVNISAATSLILWKSDESSSYTYKIH 402
DB 276 CSVWVEKGVNSSSWRLVSTTAPRPNVLEAQNTSSIALTWEPDGPDPQNSTYGV 335
QY 403 VAGETDSNINWSEBRAVYIPGLSSTFNITVCPVLGDIESTPFLQYH----- 451
DB 336 YTGDDGRA-----GTRSTAHNTITVDRL-----EPCLLYFVSVWVGKNGINS 377
QY 452 -----TPPVVSDFRVTVVSTTEIGLAWSSHAD-----SPQMHTQGAQNSRVEI 498
DB 378 SRETNATTAAPNPNRNLHMETQNTSSIALCWEVVDGYPQDYTYWVGITGDG--GGETRN 436

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